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(54) Title: BIALLELIC MARKERS (57) Abstract		
The invention provides nucleic acid segments of the hybridizing to regions flanking these sites are also provided paternity testing, medicine and genetic analysis.	e humar d. The r	n genome including polymorphic sites. Allele-specific primers and probes nucleic acids, primers and probes are used in applications such as forensics,
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BIALLELIC MARKERS

RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/030,455, filed November 6, 1996, 5 the entire teachings of which are incorporated herein by reference.

BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution,

10 generating variant forms of progenitor sequences (Gusella, Ann. Rev. Biochem. 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism

25 (RFLP) Is a variation in DNA sequence that alters the length of a restriction fragment (Botstein et al., Am. J. Hum. Genet. 32, 314-331 (1980)). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment.

RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; WO90/11369; Donis-Keller, Cell 51, 319-337 (1987); Lander et al., Genetics 121, 85-99 (1989)). When a heritable trait can be linked to a particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the animal will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra10 nucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR)

polymorphisms. VNTRs have been used in identity and paternity analysis (US 5,075,217; Armour et al., FEBS Lett. 307, 113-115 (1992); Horn et al., WO 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Some single nucleotide polymorphisms occur in protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective or other variant protein and, potentially, a genetic disease. Examples of genes, in which polymorphisms within coding sequences give rise to genetic disease include β-globin (sickle cell anemia) and CFTR (cystic fibrosis). Other single nucleotide polymorphisms occur in noncoding regions. Some of these polymorphisms may also result in defective protein expression (e.g., as a result of defective splicing). Other single nucleotide

Single nuclectide polymorphisms can be used in the same manner as RFLPs and VNTRs, but offer several advantages.

Single nuclectide polymorphisms occur with greater

frequency and are spaced more uniformly throughout the
genome than other forms of polymorphism. The greater
frequency and uniformity of single nucleotide polymorphisms
means that there is a greater probability that such a

5 polymorphism will be found in close proximity to a genetic
locus of interest than would be the case for other
polymorphisms. The different forms of characterized single
nucleotide polymorphisms are often easier to distinguish
than other types of polymorphism (e.g., by use of assays
employing allele-specific hybridization probes or primers).

Only a small percentage of the total repository of polymorphisms in humans and other organisms has been identified. The limited number of polymorphisms identified to date is due to the large amount of work required for their detection by conventional methods. For example, a conventional approach to identifying polymorphisms might be to sequence the same stretch of DNA in a population of individuals by dideoxy sequencing. In this type of approach, the amount of work increases in proportion to both the length of sequence and the number of individuals in a population and becomes impractical for large stretches of DNA or large numbers of persons.

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SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a polymorphic site. Complements of these segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying the polymorphic site in the segments can be the reference (Table, column 3) or an alternative base (Table, column 4).

The invention further provides allele-specificoligonucleotides that hybridize to a segment of a fragment
shown in the Table, column 7, or its complement. These
15 oligonucleotides can be probes or primers. Also provided
are isolated nucleic acids comprising a sequence shown in
the Table, column 7, or the complement thereto, in which
the polymorphic site within the sequence is occupied by a
base other than the reference base shown in the Table,
20 column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases present at the polymorphic sites in the individuals tested.

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DETAILED DESCRIPTION OF THE INVENTION DEFINITIONS

An oligonucleotide can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally 5 occurring or synthetic, but are typically prepared by synthetic means. The oligonucleotides of the present invention can comprise all of an oligonucleotide sequence presented in column 7 of the Table or a segment of such an oligonucleotide which includes a polymorphic site. 10 Oligonucleotides can be all of a nucleic acid segment as represented in column 7 of the Table; a nucleic acid sequence which comprises a nucleic acid segment represented in column 7 of the Table and additional nucleic acids (present at either or both ends of a nucleic acid segment 15 of column 7); or a portion (fragment) of a nucleic acid segment represented in column 7 of the Table which includes a polymorphic site. Preferred oligonucleotides of the invention include segments of DNA, or their complements, which include any one of the polymorphic sites shown in the 20 Table. The segments can be between 5 and 250 bases, and, in specific embodiments, are between 5-10, 5-20, 10-20, 10-50, 20-50 or 10-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in the Table.

Hybridization probes are oligonucleotides which bind in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., Science 254, 1497-1500 (1991).

As used herein, the term primer refers to a singlestranded oligonucleotide which acts as a point of
initiation of template-directed DNA synthesis under
appropriate conditions (e.g., in the presence of four
different nucleoside triphosphates and an agent for

polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 5 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template. 10 The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) -primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with 15 the complement of the 3' end of the sequence to be amplified.

As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same

20 chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats,

and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic or biallelic polymorphism has two forms. A triallelic polymorphism has three forms.

10 A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. -The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another 20 pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Typically the polymorphic site is occupied by a base other than the reference base. For example, where the reference allele contains the base "T" at the polymorphic site, the altered allele can contain a "C", "G" or "A" at the polymorphic site.

Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

conditions, are suitable for allele-specific probe
hybridizations. Equivalent conditions can be determined by
varying one or more of the parameters given as an example,
as known in the art, while maintaining a similar degree of
identity or similarity between the target nucleotide
sequence and the primer or probe used.

The term "isolated" is used herein to indicate that the material in question exists in a physical milieu distinct from that in which it occurs in nature. For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstance, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all

I. Novel Polymorphisms of the Invention

The novel polymorphisms of the invention are listed in the Table. The first column of the Table lists the names assigned to the fragments in which the polymorphisms occur.

The fragments are all human genomic fragments. The sequence of one allelic form of each of the fragments (arbitrarily referred to as the prototypical or reference form) has been previously published. These sequences are listed at http://www-genome.wi.mit.edu/ (all STS's (sequence tag sites)); http://shgc.stanford.edu (Stanford STS's); and http://www.tigr.org/ (TIGR STS's). The Web sites also list primers for amplification of the fragments,

and the genomic location of fragments. Some fragments are expressed sequence tags, and some are random genomic fragments. All information in the websites concerning the fragments listed in the Table is incorporated by reference in its entirety for all purposes.

The second column lists the position in the fragment in which a polymorphic site has been found. Positions are numbered consecutively with the first base of the fragment sequence as listed in one of the above databases being 10 assigned the number one. The third column lists the base occupying the polymorphic site in the sequence in the data base. This base is arbitrarily designated the reference or prototypical form, but it is not necessarily the most frequently occurring form. The fourth column in the Table 15 lists the alternative base(s) at the polymorphic site. The fifth column of the Table lists a 5' (upstream or forward) primer that hybridizes with the 5' end of the DNA sequence to be amplified. The sixth column of the Table lists a 3' (downstream or reverse) primer that hybridizes with the 20 complement of the 3' end of the sequence to be amplified. The seventh column of the Table lists a number of bases of sequence on either side of the polymorphic site in each fragment. The indicated sequences can be either DNA or RNA. In the latter, the T's shown in the Table are 25 replaced by U's. The base occupying the polymorphic site is indicated in EUPAC-IUB ambiguity code.

II. Analysis of Polymorphisms

A. Preparation of Samples

polymorphisms are detected in a target nucleic acid
from an individual being analyzed. For assay of genomic
DNA, virtually any biological sample (other than pure red
blood cells) is suitable. For example, convenient tissue

samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. See generally PCR Technology:

10 Principles and Applications for DNA Amplification (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); PCR Protocols: A Guide to Methods and Applications (eds. Innis,—et-al., Academic Press, San Diego, CA, 1990); Mattila et al., Nucleic Acids Res. 19, 4967 (1991); Eckert et al., PCR

15 Methods and Applications 1, 17 (1991); PCR (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, Genomics 4, 560 (1989), Landegren et al., Science 241, 1077 (1988),

20 transcription amplification (Kwoh et al., Proc. Natl. Acad. Sci. USA 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., Proc. Nat. Acad. Sci. USA, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification

25 methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

30 B. Detection of Polymorphisms in Target DNA
There are two distinct types of analysis of target DNA
for detecting polymorphisms. The first type of analysis,

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sometimes referred to as de novo characterization, is carried out to identify polymorphic sites not previously characterized (i.e., to identify new polymorphisms). This analysis compares target sequences in different individuals 5 to identify points of variation, i.e., polymorphic sites. By analyzing groups of individuals representing the greatest ethnic diversity among humans and greatest breed and species variety in plants and animals, patterns characteristic of the most common alleles/haplotypes of the 10 locus can be identified, and the frequencies of such alleles/haplotypes in the population can be determined. Additional allelic frequencies can be determined for subpopulations characterized by criteria such as geography, race, or gender. The de novo identification of 15 polymorphisms of the invention is described in the Examples section. The second type of analysis determines which form(s) of a characterized (known) polymorphism are present in individuals under test. There are a variety of suitable procedures, which are discussed in turn.

Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., Nature 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe

hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

15 2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in WO 95/11995. One form of such arrays is described in the Examples section in connection 20 with de novo identification of polymorphisms. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray 25 contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described in the Examples, except that the probes exhibit complementarity to 30 the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference

sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

3. Allele-Specific Primers

An allele-specific primer hybridizes to a site on 5 target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, Nucleic Acid Res. 17, 2427-2448 (1989). This primer is used in 10 conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows 15 a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of 20 the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

4. Direct-Sequencing

The direct analysis of the sequence of polymorphisms of
the present invention can be accomplished using either the
dideoxy chain termination method or the Maxam Gilbert
method (see Sambrook et al., Molecular Cloning, A
Laboratory Manual (2nd Ed., CSHP, New York 1989); Zyskind
et al., Recombinant DNA Laboratory Manual, (Acad. Press,
1988)).

- 5. Denaturing Gradient Gel Electrophoresis
 Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., PCR Technology, Principles and Applications for DNA Amplification, (W.H. Freeman and Co, New York, 1992), Chapter 7.
- 6. Single-Strand Conformation Polymorphism Analysis 10 Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, 15 as described in Orita et al., Proc. Nat. Acad. Sci. 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Singlestranded nucleic acids may refold or form secondary 20 structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

25 III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

A. Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See 5 generally National Research Council, The Evaluation of Forensic DNA Evidence (Eds. Pollard et al., National Academy Press, DC, 1996). The more sites that are analyzed, the lower the probability that the set of polymorphic forms in one individual is the same as that in 10 an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with -polymorphisms in distal genes. Preferred polymorphisms for use in forensics are biallelic because the population 15 frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic 20 analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of 25 polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime 30 scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a

match of suspect and crime scene sample would occur by chance.

p(ID) is the probability that two random individuals have the same polymorphic or allelic form at a given

5 polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies x and y, the probability of each genotype in a diploid organism is (see WO 95/12607):

10 Homozygote: p(AA) = x²
Homozygote: p(BB) = y² = (1-x)²
Single Heterozygote: p(AB) = p(BA) = xy = x(1-x)
Both Heterozygotes: p(AB+BA) = 2xy = 2x(1-x)

The probability of identity at one locus (i.e, the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation: $p(ID) = (x^2)^2 + (2xy)^2 + (y^2)^2.$

These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity p(ID) for a 3-allele system where the alleles have the frequencies in the population of x, y and z, respectively, is equal to the sum of the squares of the genotype frequencies:

25 $p(ID) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$ In a locus of n alleles, the appropriate binomial expansion is used to calculate p(ID) and p(exc).

The cumulative probability of identity (cum p(ID)) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus.

cum p(ID) = p(ID1)p(ID2)p(ID3)...p(IDn)

The cumulative probability of non-identity for n loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

cum p(nonID) = 1-cum p(ID).

If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

10 B. Paternity Testing

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced.

- 15 Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.
- If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him

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incompatible as the father) is given by the equation (see WO 95/12607):

p(exc) = xy(1-xy)

where x and y are the population frequencies of alleles A 5 and B of a biallelic polymorphic site.

(At a triallelic site p(exc) = xy(1-xy) + yz(1-yz) +xz(1-xz) + 3xyz(1-xyz))), where x, y and z and the respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

p(non-exc) = 1-p(exc)10

> The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

cum p(non-exc) = p(non-exc1)p(non-exc2)p(non-exc3).... 15 p(non-excn)

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded)

cum p(exc) = 1 - cum p(non-exc).

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's 25 polymorphic marker set attributable to his/her father.

C. Correlation of Polymorphisms with Phenotypic Traits The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and 30 contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the

circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert 5 phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulimenia, diabetes insipidus, Lesch-Nyhan 15 syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos 20 syndrome, osteogenesis imperfecta, and acute intermittent porphyria). Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous 25 system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers 30 of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance

(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of 5 individuals who have been tested for the presence or absence of a phenotypic trait of interest and for polymorphic markers sets. To perform such analysis, the presence or absence of a set of polymorphisms (i.e. a polymorphic set) is determined for a set of the 10 individuals, some of whom exhibit a particular trait, and some of which exhibit lack of the trait. The alleles of each polymorphism of the set are then reviewed to determine whether the presence or absence of a particular allele is associated with the trait of interest. Correlation can be 15 performed by standard statistical methods such as a κ squared test and statistically significant correlations between polymorphic form(s) and phenotypic characteristics are noted. For example, it might be found that the presence of allele Al at polymorphism A correlates with 20 heart disease. As a further example, it might be found that the combined presence of allele A1 at polymorphism A and allele B1 at polymorphism B correlates with increased milk production of a farm animal.

Such correlations can be exploited in several ways. In
the case of a strong correlation between a set of one or
more polymorphic forms and a disease for which treatment is
available, detection of the polymorphic form set in a human
or animal patient may justify immediate administration of
treatment, or at least the institution of regular
monitoring of the patient. Detection of a polymorphic form
correlated with serious disease in a couple contemplating a
family may also be valuable to the couple in their
reproductive decisions. For example, the female partner

might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified.

Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered. Each production trait was analyzed individually with the following animal model:

 $Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \dots \beta_{17} + PE_n + a_n + e_p$ where Y_{ijknp} is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy record; μ is an overall mean; YS_i is the effect common to all cows calving in year-season; X_k is the effect common to cows in either the high or average selection line; β_1 to β_{17} are the binomial regressions of production record on mtDNA

D-loop sequence polymorphisms; PE_n is permanent environmental effect common to all records of cow n; a_n is effect of animal n and is composed of the additive genetic contribution of sire and dam breeding values and a

5 Mendelian sampling effect; and e_p is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used as parents for breeding the next generation of the herd.

D. Genetic Mapping of Phenotypic Traits

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present 15 section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such 20 analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., Proc. Natl. Acad. Sci. (USA) 83, 7353-7357 (1986); Lander et al., Proc. Natl. Acad. Sci. (USA) 84, 25 2363-2367 (1987); Donis-Keller et al., Cell 51, 319-337 (1987); Lander et al., Genetics 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, Med. J. Australia 159, 170-174 (1993); Collins, Nature Genetics 1, 3-6 30 (1992).

Linkage studies are typically performed on members of a family. Available members of the family are characterized

for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers cosegregate with a phenotypic trait. See, e.g., Kerem et al., Science 245, 1073-1080 (1989); Monaco et al., Nature 316, 842 (1985); Yamoka et al., Neurology 40, 222-226 (1990); Rossiter et al., FASEB Journal 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the 10 odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction θ , versus the situation in which the two are not linked, and thus segregating independently (Thompson & 15 Thompson, Genetics in Medicine (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in The Human Genome (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions (θ) , 20 ranging from θ = 0.0 (coincident loci) to θ = 0.50 (unlinked). Thus, the likelihood at a given value of θ is: probability of data if loci linked at θ to probability of data if loci unlinked. The computed likelihoods are usually expressed as the log_{10} of this ratio (i.e., a lod For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod 30 scores for differing values of θ (e.g., LIPED, MLINK

(Lathrop, Proc. Nat. Acad. Sci. (USA) 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See

Smith et al., Mathematical tables for research workers in human genetics (Churchill, London, 1961); Smith, Ann. Hum. Genet. 32, 127-150 (1968). The value of θ at which the lod score is the highest is considered to be the best estimate of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of θ) than the possibility that the two loci are unlinked. By convention, a combined lod score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared.

Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

IV. Modified Polypeptides and Gene Sequences

The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some

15 nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component)

10 except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the

corresponding codon in any of the alternative forms shown in the Table.

Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include 20 fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, supra. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as 25 E. coli, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, e.g., mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing 30 includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, i.e., 80, 95 or 99% free of cell component contaminants, as described in Jacoby,

5 Methods in Enzymology Volume 104, Academic Press, New York (1984); Scopes, Protein Purification, Principles and Practice, 2nd Edition, Springer-Verlag, New York (1987); and Deuischer (ed), Guide to Protein Purification, Methods in Enzymology, Vol. 182 (1990). If the protein is

10 secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene 15 and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating 20 the Mouse Embryo, A Laboratory Manual, " Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, Science 244, 1288-1292 25 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate

the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to 10 corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptidefragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, Antibodies, A 15 Laboratory Manual, Cold Spring Harbor Press, New York (1988); Goding, Monoclonal antibodies, Principles and Practice (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of 20 immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

V. Kits

The invention further provides kits comprising at least one allele-specific oligonucleotide as described above.

Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10,

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100 or all of the polymorphisms shown in the Table.

Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the methods.

The following Examples are offered for the purpose of illustrating the present invention and are not to be construed to limit the scope of this invention. The teachings of all references cited herein are hereby incorporated herein by reference.

EXAMPLES

The polymorphisms shown in the Table were identified by resequencing of target sequences from three to ten unrelated individuals of diverse ethnic and geographic backgrounds by hybridization to probes immobilized to

20 microfabricated arrays or conventional sequencing. The strategy and principles for design and use of such arrays are generally described in WO 95/11995. The strategy provides arrays of probes for analysis of target sequences showing a high degree of sequence identity to the reference sequences of the fragments shown in the Table, column 1. The reference sequences were sequence-tagged sites (STSs) developed in the course of the Human Genome Project (see, e.g., Science 270, 1945-1954 (1995); Nature 380, 152-154 (1996)). Most STS's ranged from 100 bp to 300 bp in size.

A typical probe array used in this analysis has two groups of four sets of probes that respectively tile both strands of a reference sequence. A first probe set

comprises a plurality of probes exhibiting perfect complementarily with one of the reference sequences. Each probe in the first probe set has an interrogation position that corresponds to a nucleotide in the reference sequence. 5 That is, the interrogation position is aligned with the corresponding nucleotide in the reference sequence, when the probe and reference sequence are aligned to maximize complementarily between the two. For each probe in the first set, there are three corresponding probes from three 10 additional probe sets. Thus, there are four probes corresponding to each nucleotide in the reference sequence. The probes from the three additional probe sets are identical to the corresponding probe from the first probe set except at the interrogation position, which occurs in 15 the same position in each of the four corresponding probes from the four probe sets, and is occupied by a different nucleotide in the four probe sets. In the present analysis, probes were 25 nucleotides long. Arrays tiled for multiple different references sequences were included 20 on the same substrate.

Multiple target sequences from an individual were amplified from human genomic DNA using primers for the fragments indicated in the listed Web sites. The amplified target sequences were fluorescently labelled during or 25 after PCR. The labelled target sequences were hybridized with a substrate bearing immobilized arrays of probes. The amount of lable bound to probes was measured. Analysis of the pattern of label revealed the nature and position of differences between the target and reference sequence. For example, comparison of the intensities of four corresponding probes reveals the identity of a corresponding nucleotide in the target sequences aligned with the interrogation position of the probes. The

corresponding nucleotide is the complement of the nucleotide occupying the interrogation position of the probe showing the highest intensity (see WO 95/11995). existence of a polymorphism is also manifested by 5 differences in normalized hybridization intensities of probes flanking the polymorphism when the probes hybridized to corresponding targets from different individuals. For example, relative loss of hybridization intensity in a "footprint" of probes flanking a polymorphism signals a 10 difference between the target and reference (i.e., a polymorphism) (see EP 717,113). Additionally, hybridization intensities for corresponding targets from different individuals can be classified into groups or clusters suggested by the data, not defined a priori, such 15 that isolates in a give cluster tend to be similar and isolates in different clusters tend to be dissimilar. Hybridizations to samples from different individuals were performed separately. The Table summarizes the data obtained for target sequences in comparison with a 20 reference sequence for the individuals tested.

From the foregoing, it is apparent that the invention includes a number of general uses that can be expressed concisely as follows. The invention provides for the use of any of the nucleic acid segments described above in the diagnosis or monitoring of diseases, such as cancer, inflammation, heart disease, diseases of the CNS, and susceptibility to infection by microorganisms. The invention further provides for the use of any of the nucleic acid segments in the manufacture of a medicament for the treatment or prophylaxis of such diseases. The invention further provides for the use of any of the DNA segments as a pharmaceutical.

All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and individually indicated to be so incorporated by reference.

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				TGTGAAACTCCACTTGAAGCCAAAGAAAGAAACTCACACTTAAAACACATGCCAGTTGGGAAGGTCT
				GAAAACTCAGTGCATAATAGGAACACTTGAGACTAATGAAAGAGAGAG
				GTACTGGCCAAATACTGAATAAACAGTTGAAGGAAAGACATTGGAAAAAGCTTTTGAGGATAATG!
WI-7070	226 CT	:		TACTAGACTTTATGCCATGGTGTTTC/T/AGTTTAATGCTGTGTCTCTGTCAG
				AAGCCATTGACGTAACATCTCAGAGGTTATTTGCATGGATTGACTCCTGGGACAAAAGGAC[G/CJAA
				AAACACTCTTCTGTGGATATCTGTGCAGATAGATGACCCAAAGATCAGATGCTACCCAGATGTGTTTT
				GATAATACATAAGCCCCTAGGATTTAGATACAATCTTGAAAGAAA
WI-10744	616	 0	:	AAATGAGGTAAAGTTTCAGGCACTCA
				GGGCAAATTACCAGCAAAAAGTCAAATTACCAGCATCAAAGTCAGGTGCAAAGGAGGTAGAACAA
	_			TTACAGTAACTATGTCAATCTTTTGTTATATTAGTATTATCTGCCCAATGCCTAGAATACCTAGTG
				GGTCCCTAATAGTTATTAGTTCCTTTTTTTTTTTTTTTT
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			_	AGTAGTGCCAATTCTTCAGGTCTCTTTGAATTTTTCTCTGCTATTGAGGACATTTCCACTTTCTACTACT
WI.5222	52	::-	:	TCTCGACTCTATAACAACTCCAACAGAA
				TATGCACTTCCACAAAAGCGATATAATTTAAAAGTTTTTTCATTAGAAATAAAT
_				ATATGITATTATAGGCATTTATTACTAACTATAGTCCTTCTTGGAAGGAA
				ATAAAGTACATGTAATTTATAGTAACATATTTACTATATACATATGGAAAAAATCATATCTCACA
WI-8007	242	-:- V	.:	GAAGAGCTGAACAGACATTCACCAGGATACGACTGTTGGAC[C/A]AGCTGCTG
				TCAGTTGCAAAAATTGCTGCCATAAACATGCTTTGCTTATCTCTGTGCATATGTATG
				TCTATATTCACACATATGAGTGAAATTTCJC/TJGGGGCATGGGAAATACATCTTTATGAGACATTGA
		_		ACTGCTCACCACTATCATAGTATCCATTTAAACAGACCAACAATGTATAAGAAIICCCIIIGIIIIAC
WI-9823	97.CT	CT		ATGCTTTCCAATCTGATTTTGTATGACTATTGTATGCACAGI

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I COR-IM	5			GTGACCTTCCTGCAGCGTGGAGATGGCACATCCTTGCTGCTGGGGACTTGGCCCTGCTATTTATT
				TATTTATGTCTTAATCTCTTCCACTGATGCATCCTCCAAGGGTAGATGGGGAGGGGTCTGTGTGAAGGG
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				CATCTGGCCCTITTTTGAGTTTTGAATATTTTTGT[GAJTGACTCCTATGCACATGATAAATTTTTTTTTTTTTTT
				TGCTTGTCTCTTATCTTTTGTTATAGGAGTTTTGGCCATGACCCIIIAIGAGGAGGAAAAAGGAG
WI-10072 105 GA	105 GA	;	•	TCACCCCCTTTTGCCTCTACAACCTTATAGATAT11AAA1A1C1111
				TTGGTGTGAACTCAGAATATAGGGAAAATAAGACAATTTGAA[T/A,C]GTACCCCAGGAAACAAGAG
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9866-IM	42 T C-	,	1	ATATCAATAGCATGCATATGGGGTGTTGGATTCTTAGAACITAITGCAATT
				GTCTATTGCAGGAGAAACGTCCCTTGCCACTCCCCACTCTCATCAGGCCAAGTGGAGGACTGGCCAGA
				GGGCCTGCACATGCAAACTCCAGTCCCTGCCTTCAGAGAGCTGAAAAGGGTCUCICUGGICTTTTTTTTTTTTTTTTTTTTTTTTTT
				CAGGCTTTGCATGCGCTCTATTCCCCCTCTGCTCTCCACCTTCTTTGCATCTTTGCATGCA
WI-7041	174 CA-			AGCTGTATTGTAACAAGCTCATTTGTACAGTGTCTGTTCATGIAAIAA
i				ATAAACCCTTGTGTATGTATCACCCAACTCACTAATTATCAACTTATGTGCTATCAGATATCCLCLCL
				ACCCTCACGTTATTTTGAAGAAATCCTAAACATCAAATACTTTCATCCATAAAAATGTCAATTTT
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				TCTTATTIGCATTICACAGIAGCCCCAIGAAGIAGGIATAACCAGCCTCTATTITAACATGAGAAGAT
				CCCTGGCTTCCTGACTCCAAAGCTTATCCCTTCTCTTCT
WI-10826	132 A C		:	GAAAGCCCAGCCTCTCCATCCCCAC
				AGATCTGCCATTAGTATTTATTCCTTTGAAGATACTTTGGAGATTCATTTTCTTGAGTGGCACTGCAT
				GCTCATTCAGTGAAAACTTGTGGGGTATAGAAATGGAATGGAGAGTTTCAAACAGCTTTGCTGAAAC
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WI-1021	24 A T		:	AATTGGACAGTTTTGGTTTCCAC
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				TTTCAATAAAAAGAGTGACATGAATTGAACATGTGTTTTAGATAAAGGGCACTT[G/T]GCAGGAGTGT
				TTAGGATGAAGAGAGAAGAGATTAAGGAAGATCAGGAAGAAAAGTAGCAATGGAATGAAAATAG
WI-4687	121 GT			GAGGCCCTGAGATCACTGGATAATCTAAAAACCAAGAGAAAGAA
		:		TTCATTTCCCTTCCAAAATCCTTAGGAAATTTTACATTATGGGCTAGTGCTTTGGGTGTGAGCGGATT
				ATGTCTGACGCCATGGGTGTTCATAAGTGACTTGAGAGTTT/GJACTGTAGAGGCTACACAGAAATCT
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WI-4719h	WI.4719h 107 T G		<u>;</u>	TGCTCAAAATTCCCCACTTGTCAACTTATCCTTAAGACATTTTCACAGGA
				TTCATTTCCCTTCCAAAATCCTTAGGAAATTTTACATTATGGGCTAGTGCTTTGGGTGTGAGCGGATT
				ATIG/AITCTGACGCCATGGGTGTTCATAAGTGACTTGAGAGTTACTGTAGAGGCTACACAGAAATCT
				CTGTGAGGGGCATGTAATTGTATTCATTCAACAATTCTGCTATGCTTCTCAGATTGCAGAAAAATCAC
WI-4719	70GA		1	TGCTCAAAATTCCCCACTTGTCAACTTATCCTTAAGACATTTTTCACAGGA
				TCAACACGCTTTTATTGCCACTTCTGGCTCCCCTCGTCCCAGCAAGATTCCTACCTCTTACCCTGTAGG
				AATACTGAGCTCCGATGCAGGGGAATGGGGTGGTGGGGGTGTTACCACTTCTCCTCTGCACACTGCCAAGT
				TAAAGAAAACCCTGCTTGCTGGAGAGAGAGAGACAGAGAGAG
WI-9484b	216 GC			AGTCCCACTTCT[G/C]ACTGCAGAGTATAGGGACCAGGGTTCCAAACTTT
			-	TCAACACGCTTTTATTGCCACTTCTGGCTCCCCTCGTCCCAGCAAGATTCCTACCTTACCCTGTAGG
				AATACTGAGCTCCGATGCAGGGAATGGGGTGGGGGTGTTACCACTTCTCCTCTGCACACTGCCAAGT
				TAAAGAAAACCCTGCTTGCTGGAGAGAGAGGGCCAGACAGG(G/A)AGGAATTCAAGGCATGTATG
WI-9484	WI-9484 178 GA		-	GCTCAGTCCCACTTCTGACTGCAGAGTATAGGGACCAGGGTTCCAAACTT

	. —		AGGATGGAAGGAGACGGGGCAGGAGAAACTCTCTTCTGCTAAATCGATAGGAGTCAGTTTTGTTTTTTTT
	-		TAAATGCTGACTACAGCCACTGACATGGTTGGCTGAAATTTACTAAAGAAAAATAACTGAAAAGATAACTGAAAAGATTAAAAG
		-	GTGACACAAGAAGICATIAGIAGITIGATAATGCTTCCAAACTGTAGCTGTCACAG
WI-/ 330			TTAAAAACACTTCAGGTTGGTGAAGCAGAAAAGGGGATGTGATTACAATTTAAATGAATCAGTCACTT
			GCACAATTAATCCTCTTGGCATCATACAAACTGGGTTTTAATGGCAAATGATGACATCATAGCATGA
			CCAACACTCATGGAAGGCAGTCTAGAGTCCATCACGCTCACACCTGAGGGGAAGGCACTGCACCCA
WI-0443	211GA	. :	CTGACGAGACIGAJCAGAGACCTTGGACTACAGATGACACCACATGCCCCACTT
2			TCTCTCAAAAGAGAAAAACCCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTAIC/TJGGAT
			CATCAACAAGATTTCCTTGTGCAAAATATTTGACTATTCTGTATCTTTCATCCTTGACTAAATTCGTG
			ATTTCAAGCAGCATCTTCTGGTTTAAACTTGTTGCTGTGAACAATTGTCGAAAAGAGICTTCCAAT
WI.7166	59 C T	:	TAATGCTTTTTATATCTAGGCTACCTGTTGGTTAGATTCAAGGCCCCGAG
			GCTTCTTCCCCAGGAAGCGGGGTCTTGGCCTGGAACCTTCCAGAGAGGAGGAGGAGGAGCAATTTAGCC
			CARCCTECTCCCATCTGCCCCCTGCAACAGCTGCAGGCTGCTTCCTCTCTCT
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			GTACTITIAGGCCTGTGGAGGGTGGGCATTTAGTGGTGACCCTTGCACCAGGGTTTTCTAACAGATGAC
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			TCAGITCTAGICTCTCTGGGGCCACACACAGAAACTCTTTTGGGCTQT7CJTTTTTCTCCCTCTGGATCA
			AAGTAGGCAGGACCATGGGACCAGGTCTTGGAGCTGAGCCTCTCACCTGTACTCTTCGGAAAAAICCI
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			CTGGGGGAGGGCCTCCCCTIG/ACCCTGATCATGTCTACCTAACTGCCTACTCTTAACAACTGCTACTGTTAACTAAC
			TGTGGTATGGGGATCCTAAGCCAAAAAGCTGAAATGAACATGTICIAGCACIACAAAAAICCAIACI
WI-563	87 GA	_;	GCCCTCAGTAAAGGCAAATTTTAAATCTCTTTGGATAACCCAGGGCACAT

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				GGATGACTTACCCAATAGCAGGGTGGGTACATTCATGGGTAACAACACCCTGGACTGGGATGGCAGA
				GACATCCACCTTAGCAAAGTGGGGGCTJACCTAGTTAGAGCAGTGGAGTACCCTGAGTACGACCCCC
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					COCCACCTCTCACCACTTAGAAAAGGGCATTTCAAGCACATTCAATGAGGCTTCATATACTGGTTAGC
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					CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTCAGCTTTCCCTGCCACATCCAGGTTGTTGTCC
					CAATGAAATACTGAGATGCTGGGCTGTCTCTCCCTTCCAGGAATGCTGGGCCCCCAGCCTGGCCAAACAC
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				CATTTGGTGGAGAGATTTACAAGGTTAAGATCATGTGTCCATCAAAGTGCAATCCTATCAATCA
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			CTCCCCCACACACACACAATACAGAGATT[G/C]AATTCAGGAGCCAGIII LIAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
WI-234	165 G C		AATCATACACAGIAAICICITIGGIGCITTAGITTICICAAATCATCTAATCT
			AGCTTTTGAAATCCAAAAACCACATJA/GJCTTGACTCTCTTTTGAACGCATGGGGGGGGGGGGGGGG
			CICIANGE AGAMAN INCAMAN CONTROLL CONTROL CONTROLL CONTROL
1020	U		TCTGGCAAGGCTTTGTCTTATCCTCCTTGCTATCCCTGATGACTGGGCAAA
00/2-(M	1		

			AGCTTTTGAAATCCAAAAACCACATAAGCTTGAACTCTCTTATCCTCCTTGTTGTAACATCTATCC
			CIGACATGAAAAAIACAAAAGCATCTCTCTGAAAAAACCTCTCCTGAAAGACATGAGCTATTAGGAGC
WI.276	25 AlG		TCTGGCAAGGGCTTTGTCTTATCCTCCTTGCTGATGACTGGGCAAA
			TTTCCCAATCCACAGGTAAAACTAATATAGATGTATAGAATTTAGAACTACTTCCGGAJGTTT
			TTCCCTGGGGAAAATATTCACAAAACATTTGTGGTCTGCAATCAGGTTAAAAGACATAGTGTGCCA
			TTTGTCATCAGACAGGTAGAGGCCTGACTCTGGCAGGATTAGCTACCACTAGCTGTGAGACTTAGGT
WI.427	59 G A	:	ATTCATTTATTAGAGCCAGGGTCTTGCTCTGCCCAGCTTTCAGTGCAGT
			CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAAGCCCAGAAAGGAAGCCTGTCTC
			AATACACTAGATATAGTTACTGTGATTATATATTTTAATTCJAAATGGTCCTTTTATTAAAAAAAA
			AAAAGNTATCTAAAGAGAAAACCATAATAATCTCTCAGGTAATTATGGCCACAGCCAAAACCAGTCT
200	1 00	_;	TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATACTTCTCCACTTCC
770C-IM	S:		CTCTTCACTCCAGAACACTATAGCTTACTTAATGGTTACAGATTAAGCCCAGAAAGGAAGCCTGTCTC
_			AATACACTAGATATAGTTACTGTGATTATATATTTTAA(T/C)AAATGGTCCTTTTATTAAAAAAAA
_			AAAACNTATCTAAAGGGGAAAACCATAATAATCTCTCAGGTAATTATGGCCACAGCCAAAACCAGTCT
	- i		TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562b	300	-	CTCTTCACTCCACACACTATATTGCTTAATGGTTACAGATTAAGCCCAGAAAGGAAGCCTGTCTC
		_	A A TACACTAGA TATACTG TG TG TATATATTTTTC JAATAAATGG TCCTTTTATTAAAAAAAA
		_	AAAAGNTATCTAAAGAGAAAACCATAATAATCTCTCAGGTAATTATGGCCACAGGCAAAACCAGTCT
200			TICTAAACCTAAAGACTCTCATAAAGGCCCTATCACATACTTCTCCACTTCC
79C-IM	21 22		CTOTA A THE CASE OF THE CASE O
			ATGAGGAAGAAGAGGGNGTAAGAAACAAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT
			GATACATGIA/GITAATGACCCTCCATGACTCTGGTACCTCATCATTACCAATGTGAGAATTATTAAC
2000			TTGATCTAATATCTTCACAACTAATATACCTGAGAGAATAAGTCTATTTAAT
0/6C-IM	5		CTGTAATTTGGTGGCTTTGCAACTTTTCCCACAGTAACCTTTAGAATNTNAAAGGTGGAAGGTAAGG
			ATGAGGAAGAGGGGNGTAAGAACAAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT
			GATACATGIA/GITAATGACCCTCCATGACTCTGGTACCTCATCATTACCAATGTGAGAATTATTAAC
44,607	141 4	i,	TTGATCTAATATTCTTCACAACTAATATACCTGAGAAATAAGTCTATTTAAT
		-	GTGTAATTTGGTGGCTTTGCAACTTTTCCCACAGTAACCTTTAGAATNTNAAAGGTGGAAGGTAAGG
			ATGAGGAAGAGGGGNGTAAGAAACAAAAGATGTCTATGTTGAAGAAGTATCCTTAGGAIAIICI
_			GAT[AG]CATGATAATGACCCTCCATGACTCTGGTACCTCATTACTATAGTCTAATTAAT
WI-597	136 A G		TIGATCTAATATTCTTCACAACTAATATACCTGAGAGAGAGTGAGT

			TTCAAATTTAACACCATTGGGTATATTATAATTTTNGCTCTATCCATAGTTCTAACCCTCTTCTCT[G/ CACAGTGAGACACCTGCCTTCTATTGTCCTTGACGTATTAACGTATTCGATCAGTCACCCATCTGGA
WI-611	 		AOCAAGGTTTCATTTCTGCTGACCCTCCTCACCTACTTGGGCTCTGACTTCCTTGCTGGGCT GAACCTTCTCTGTGTGGCTGCCGCTTCCTCTGGGCTCCAATAC
			TGAAGCCCTCTCTCTATACCCAAGTGTCTTTATCTTAAAATGCTGTGGTGCAAGTATCTAACCCTTA
			GGGATATTGTGAGAATTCAATAGITCATACAGGGGAACATTTGGGACACAGATATATATATGTCAGA TCCATAATTGTTATAGCTATTJA/GITTATACTATGGCACCCATTTGGGACACAGATTATATATAT
WI-681b	156 AIG	•	CACCACGNATGTCCTTTAAGATATGCAGCACAAATCTGTCATGGTTT
			TGAAGCCCTCTCTCTATACCCAAGTGTCTTTATCTTAAAATGCTGTGGTGCAAGTATCTACCCTTA
			GGGATATTGTGAGAATTCAATAAGTTCATACAGGGGAAGCACTTTGTNCCTGGTATGTCATAAGCAA
			TCCATAATTGTTATAGCTATTJAGTTATACTATGGCACCATTTGGGACACAGATTATATATGTCAGA
WI-681	156 A G	::	CACCACGINATGICCITIAAGATATGCAGCACACACACACACACACACACACACACAC
			AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATTCTTTTTGGAGCCTAAGATCAGTG
			CAACCCTCCAAGGCTCCCCAGTATCTGGCACATCTTTCCCTTTTCAICTCGGGAJITTGTTTTTCC
			CAAATAATATCTCCCCCAGGGACGTCCTCTTCTAATCCCTGAAACCTGAGAAATGTTATCTTATGC
WI-867b	119 GA		AGTGCTATGGTTTGAATGTGTCCCCACAAGCACATTAGAAACTTA
			AATCITAACAGCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATTCTTTTGGAGCCTAAGATCAGTG
			CAACCCTCCAAGGCTCCCCAGTATCTGGCACATCTTTCCCTTTTCAAGTCTCCG111G1G1G1111GGC
	·		CAAATAATATCTCCCCCAGGGACGTCCTCTTCTAATCCCTGAAAACCTGAGAAAAIGITAICITAIGC
WI-867	113 A G		AGTGCTATGGTTTGAATGTCCCCCACAAGCACACATTAGAAACTTA
			AATCITAACAGCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATTCTTTTTGGAGCCTAAGATCAGTG
			CAACCCTCCAAGGCTCCCCAGTATCTGGCACATCTTTCCCTTTTCATCTCQGAJITIGIGIGITIGGC
			CAAATAATATCTCCCCCAGGGACGTCCTCTTTCTAATCCCTGAAACCTGAGAAATGTTATTGTAATCCCTGAAACCTGAGAAAATGTTATTGTAATCCCTGAAACCTGAGAAAATGTTATTGTAATCCCTGAAACCTGAGAAAATGTTATTGTAATCCCTGAAACCTGAGAAAATGTTATTGTAATCCCTGAAAACCTGAGAAAATGTTATTGTAATCCCTGAAAACCTGAGAAAAATGTTATTGTAATCCCTGAAAACCTGAGAAAAATGTTATTGTAATCCCTGAAAACCTGAGAAAAATGTTATTGTAATGCCTGAAAACCTGAGAAAAATGTTATTGTAATGCCTGAAAACCTGAGAAAAAAAA
WI-867	119 GA		AGTGCTATGGTTTGAATGTGTCCCCACAAGCACATAGAAACTTA
			TCATCAGACCTGAGATTCAGCATGAAATCTACCAAAGGTACCACAAATGTAACCTTGTCCAAAACGA
			ATCTCAGTTTCTGCATATGTAAAATGGGAATGATAAGAGCACCCACC
			GAGAGAAATAAATGAGACATTGTAAGTAAAGTTTGTAATGCACTGTTATGGCCTGAATTGTGTACCC
WI-871b	123 C		TAAAATTCATATGTTGAAGCCCTAACACCCAATATGNCTGTATTTGTACATAA
			TCATCAGACCTGAGATTCAGCATGAAATCTACCAAAGGTACCACAAATGTAACCTTGTCCAAAACGA
			ATCTCAGTTTCTGCATATGTAAAATGGGAATGATAAGAGCACCCCACCTACCT
			GAGAGAAATAAATGAGACATTGTAAGTAAAGTTTGTAATGCACTGTTATGGCCTGAATTGTGTACCC
WI-871	123 C G	:	TAAAATTCATATGTTGAAGCCCTAACACCCAATATGNCTGTATTTGTACATAA

			AGGITCTGGACTTGATGCTGGGAAACAATTGGGTNCTGGAGAATTCCTATTTGAGTNTTTCACAGAA
			CAGTAGAGCCAAATGGGAAAGGIAIUCHABIUCAIUCAIUCAICAGAGAACHNAAAAGGAATAT/CJGAACTTTAATCATGAAATGAGAACHNAAAAGGAATAT/CJGAAATGAGAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAATGAAAAATGAAAAATGAAAAATGAAAAATGAAAAATGAAAAATGAAAAATGAAAAAA
WI-884	. 198 T C	•	ATCCCGCATGCAACALLIALILAGIIGAAAAAAAAAAAAAAAAAAAAAA
			CACTTCCCAAGGGCTCTGGGGGANGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA
			CAGTGATGCCTCTCACGCCTGGCCCCCAAGAAAGTCTTNGCCAGGAAAAGCACGALGATCCTCACGAAAAAGCACGAAAAAGCACGAAAAAGCAAAAAAAA
WI-921b	205 GA	:	TCTIGAJGGGAGAGATCTGACAATTTAATCAGGAGGAAGAAGAAGAAGAGAGAG
			CACTTCCCAAGGGCTCTGGGGGANGAGCGGTGGGACACTGCCACGCGCACAGGGGACAGTTATACTGG
			TGCTTTGCTGCAGGGCLCLGULULUSANGCAGAAAAGTCTTNGCCAGGAAAAGCACGATCCATCTAC
		;	TCTIG/AJGGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATTCTTCCGAGG
WI-921	V 0 CO 2		GECTGGGATGAGAGGTCTACTTGTGGTACTGGAGGTTTCACTGGCTTGTGCTAGAGCTAGAAGTAGAAAGAA
_			GAAAGAGACAGNGATTGGCTAACGCCATGGCAGTAGTGGGCCCCCAAGGCCTGAGTAAGAAAA
			AAATCATTAGATAAATGTCTCATGACCAAAACAAGTTCAAACANTAGGIGCAGCACANNNNGGGI
		,	TTCTCTGGTCATAGAATCTCTTAAAAGGGAATCATGACAGAIIIICIIGGCIIIA
WI-9400	5000		GGCTGGGATGAGAGGTCTACTTGTGGTACTGGAGGTTTCACTGGCTTGTGCTAGAAGTAGAAA
			GAAAGAGACAGNGATTGGCTAAC(G/C)CATGGCAGTAG1GGGCCCAAAGACCACAAANNNGGGTT
			AAATCATTAGATAAATGTCTCATGACCAAAGGIICAAACAAAGAIICAAACAAATTTCTTGGCTTTA
1070		;	TTCTCTGGTCATAGAATCTCTTAAAAGGGAATCATGACAGATTTTCTCTCACTACTACTACTACTACTACTACTACTACT
WI-9430			TTGCTTCAAAGAAGTTCTTGCTCAGGAAGTTATTCATTCA
			ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGIGAATAAAGTTCTTCT
	-		CTGAGGAATTTATCAAAGATGTTAAGTTATCT[C/1]C11AGAGG1A1AAG1CA1A1AAG1CAAAG1AAG1AAG1AA
4000	T 0 12	<u>;</u>	ATGTATACTAAAGGTGGTATGGCATAAGAGTACAIA
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			ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGIGAAIAAAIGAGIGITCT
			CTGAGGAATTTATCAAAGAT[GAJTTAAGTTATCTCCTTAGAGGIAIAAGICAIAIAGGCAIAIIC
0090	155 2	<u>:</u>	ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-9008			TCCCACTGAGTATGGCTTTCAGTAGTTTTATTATGATGTGCCTAGGTACATTIGITITATTATTATGATGTGCCTAGGTACATTIGGTGTTTATTATTATTATTATTATTATTATTATTATTATT
			CGAATTGTTGTTATTACTTTGGGAAAATGCTCAACTATAAAIAIIGCIICIGAACCCIIITTACTCTCTCTCTCTCTCTCTCTCTCTCTCTC
			CTTCTTAAAGATACAAAATGTAACATTAGAACCTCTCACTAAATNTG
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			CATAGGCATATAGTACCTGTATGACTTCTATTCCAGCCACCGCAAACTTCTCCTCTCCCTGCTGGCTG
į			CTGAGCCAAAACAGGCATTTACCATAAATCACTTTGTTAGGATGAACTTATCTGGCCAAACTGATA ACAAACAATAAAAAAAAAA
WI-1147b 2	204 GA	:	
			GCATTCAGAGGGTTCGTTTAATGACATTCACTGAGGCCCTGTCTATGTCAGGCCCT I GG I G I I GAAGA CACAATCATGAACAAAAATGAAAATACAATGTGATGGTCCTCAAGTGTCTGAATGCGCCAGGTGGC
			TAAGTGCTGGGGQCTJTCTGGGGTCAGGCTGCTGGGTCACATCCTGGCTCCAAACTGCTTTGCTATG
WI-1158b 147 CT	47 CT	:	901
			GCATTCAGAGGGTTCGTTTAATGACATTCACTGAGGCCCTGTCTATGTCAGGCCCTTGGTGTTGAAGA
			CGCAATCATGAACAAAATGAAAATACAATGTGATGGTCTCCTGAGTGTCTGAATG C/G GCCAGGT
			GGCTAAGTGCTGGGGCTCTGGGGTCAGGCTGCCTGGGTCACATCCTGGCTCCAAACTGCTTTGCTATG
WI-1158a 124 C G	124 C G		(3)
			AAGTTTACAGAAAAAATACCAGAAAAGTGACTTCAAGANTCAGCTGAGATAGAAACATATGCCCA
			TCATCTTCAANGINCCCACAGACACTTATCCCTAGACAGCCATTTCTTTTGAATGN[T/C]GNCANT
			AAAAATGATTTGAAATTGGGAATAAAGCCCTCCTCTAATGATTTGACAGTGTTAGACCTTGCCTAG
WI-1304	124 T C		389
1	٠,		TTCTCAATTCCAATCTGTGTTACTTTTATTTCTTTCCATTCTATGTTGGTAAATATAAAGATG
			ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA
			TCCACTGCTTTCANTAATTNACTCCACTNATGTCTNACAAAATNACACTGTTTTAANTGNNATATG[C
WI-1305d 202 CT	202 CT	:	//JAGGGCGANGTATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
			TTCTCAATTCCAATCTGTGTTACTTTATTCTTTCTTTCCATTICTTTATGTTGGTAAATATAAAG
			ATGATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTC
			ACATCCACTGCTTTCANTAATTNACTCCACTNATGTCTNACAAAATNACACTGTTTTAANTGNNATA
WI-1305c	46 C T	:	TGCAGGGCGANGTATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
			TTCTCAATTCCAATCTGTGTGTTACTTTATTTCTTTCCATTCTATGTTGGTAAATATAAAGATG
	•		ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA
			TCCACTGCTTTCANTAA[T/C]TNACTCCACTNATGTCTNACAAAATNACACTGTTTTAANTGNNATA
WI-1305b 153 T.C	153 T.C	1	TGCAGGCCANGTAANGTATACAGNGANTCATAACAGCCCTGCCTACCA
i	! !		TTCTCAATTCCAATCTGTGTTACTTTTATTTCTTTCTTTC
			ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA
		_	TCCACTGCTTTCANTAATTNACTCCACTNATGTCTNACAAAATNACACTGTTTTAANTGNNATATGIC
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			AAU GAGGCACTOCTTIGTGAAGGCCAGTTGAAATTTATCTTCCT[A/G]GC
WI-1306D 248 A G			TTCTACATTGGAATAGTTGACTTCTATGAGNINIGCAATAATAAATGGACAATCTTGTNGINININTNG
			CACTIGGIGACTGTGCCTGGGTCATTTAGAAGCCATAGAGATGAAAGTAGCCTGCAATAAAAGAGGA
			AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGGNGAGAAGTGGCCCTNNTTTCTGATGGCTTTTCAGI
040 A00 A00 A00 A00 A00 A00 A00 A00 A00		,	CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAATTTJAGITCTTCCTAGC
			GACAAGGCTGGTACTAGTTTCCAAATTCCAAATCTATGTACACTTTCCTCTCACTTTCTCAAGGGGACA
			CATTITICISCATI AT ACT GCTTGGGGTTGGGGGGGGCAGTGGTGTGTGTTTT
			CCTACCTCTTAAATGTATCTTTNCTAATTATNATGCTAAAACCGGGTACTGTGATCTATCACTGGT1
		;	TCTTTTGGTGTTGTTGTTGCTGTTGTTTCTCCTGTAAAGNTGTTT
WI-130/0			CACAAGGCTGGTACTAGTTTCCAATTCCAAATCTATGTACACTTTCCTCTCACTTTCTCAAGTGGACA
			CATTITICISCATIATACTGCTTGGGGGTTGGGGGAGCAGTGGTGTAGGCAATIOIGTGAGATTGTCTTT
			CCTACCTCTTAAATGTATCTTTNCTAATTATNATGCTAAAACCGGGTACTGTGATCTATCACTGGTT
			TCTTTTGGTGTTGTTGTTGCTGTTGTTCCCTGTAAAGNTGTTT
WI-1307	1		CACACATOCOCA A GACA A A A GACA GAGA GA GA GA GA GA CONTOT GT GG TTTT A T C G C A G C A G C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C
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WI-1363			CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAGCTGTGTAGTGCAAGAAGTCCTGTTATTTGTAAA
			ACACCAAGTGCGGTTTAATGGAATGCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGGAAAAAUU
			CAGCGACACTATGGAGCTGAGAGTCTGTICJGAAGTTGGGTAGCTACCAGGCCTCCCAAATGTAGT
			TCTTGNGCTGAAAGTCTCTCCTTACTGAAGAGGCAATGGTTCCATCTCTAAG
WI-132/D 102			CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAGCTGTGTAGTGCAAGAAGTCCTGTTATTTGTAAA
			ACACCAAGTGCGGTTTAATGGAATGCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGGGANGACJC
			CAGCGACACTATGGAGCTGAGAGTCTGTGAAGTTGGGTAGCAGTACCAGGCCTCCCCAAATGTAGT
			TCTTGNGCTGAAAGTCTCCTTACTGAAGAGCAATGGTTCCATCTCTAAG
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				TATCAGCATGATGTGGGCTGTTGGACACAAAGTCAATTTGTACTTTTGNTGCNNNTCCTTTTGTNI ACCTAATACAATTGTTGTGGAAGATGANGTTCAAATTTGGCTTNCTTTGTTNAATTATACCCAAGG
				GAJGGATTGTGATGGTCTGTTTATTTTCCTGTGTCTTGGAACAGCAGAGTCGTCTCTGNGAGTNTG
WI-1341b 136 GA	36 GA			GTTTCAGGATTTGTCTCTGTTTCCCCAGCCCACTTGCACTTAGCAAGIGI
				CTGACAAATGTCATATCTCACTCCTAAAACCCACAGGGTCATGAAATCAGTTAGCTACCCTCAATATATG
				GCAACCCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGACCTCTCTGACCTTCTCAAA
-				GCAGGTGCTCAACAATGTAGAATTGTGAAGTACTAGATTTCAGAAATA
WI-1349e 192	92 GC	-	:	CTGACAAATGTCGTATGTCGCTCGTAAAACCCACAGGTCATAGAATCAGTTAGCTACCTCAATCCA
				GCAACCCCAGCTTTGAAATGGATGCAGGCCAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATG
		•••		GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGCTGAATTTCCATCTCTGAGTTCAAAIA
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				CTGACAAATGTCATATCTCACTCCTAAAACCCACAGGTCATAGAATCAGTTAGCTACCCTCAATCA
				GCAACCCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTCTGGTGTCTCTCAAATGAAATGCATGC
				GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGCTGAATTTCCATCTCTGAAATTTCAGTGAAATTCAGTGAAATAAAAAAAA
WI-1349c 192 GC	192 GC	;		ATAATTTGAGAAAATATGAAAATTGTGAAGTACTAGATTICAGAAAAIA
				CTGACAAATGTCATATCTCACTCCTAAAACCCCACAGGTCATAGAATCAGTTAGCTACTATATATA
				GCAACCCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCIGGCCTGTCAGTTCAAATA
				GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGCTGAAIIICCAICICIGAAIIICAAAAAAAAAA
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00401-104	5			CTGACAAATGTCATTCTCACTCCTAAAACCCACAGGTCATAGAATCAGTTAGCTACCTCAATCCA
				GCAACCCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCCTGTCAGTTGAAATA
				GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGCTGAATTTCCATCTCTGAGTTCAAGATAGTGCTGAATTTCAATTTCAGTGAAGGATAGTGCTGAATTTCAATTTCAGTGAAGGATAGTGCTGAATTTCAATTTCAGTGAAGGATAGTGCTGAATTTCAATTTCAGTGAAGGATAGTGCTGAATTTCAATTTCAGTGAAGGATAGTGCTGAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCA
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				TGGTATTTGGAATGGGGTTCAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTTG[C/J]TTCGAA
	• 			GCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGGGG
				AAAGTTTACATCAACATAATTCTTGCCCTGCATCATGCATTTGGCAATATGTCACALAGUUUUU
14035	71017		÷	TAATCCCCAAAGTGCCAAAAGGGTTGTATCTGATTTGT
	3: 3: 3:			TGGTATTTGGAATGGGGTTCAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTTGCTTCTGAA
_				TGCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGGGG
				TAAAGTTTACATCAACATAATTCTTGCCCTGCATCATGCAITIGGCAAIAIGICACAIAGCIGICAC
WI-1403	58 T C			ATAATCCCCAAAAGGCATATCTGALIIGI

				CAGGCCGGAAGAGATTCACGTGGAGAGATGT[C7]TTGGCCAGGGCGGGCAGATGTGAGCCCACGGG GGTGACAGCATGCCTGCTGGCATTTGGAGGGCCCCAGAAGGAATCCCAGTGGCCCTCTCAATGACTTG GGGTCCTCGACTTCGGAAGTTTAAGGGGCTCGGCTTCAAAAAGCTGGGTCCGGTTTGAGGCGGTTGC AGGCGAGGCCCTTAGGTCCGTATTAATGTTTGCTTTGTAAAAAGTCGC
WI-141/C		<u> </u>		CAGGCCGGAAGAGATTCACGTGGAGAGATGT[C/I]TTGGCCAGGGCGGGCAGATGTGGAGCCCACGGG
45.57				GGGTCCTCGACTTCGGAAGTTTAAGGGGCTCGGCTTCAAAAAGCTGGGTTCGGGTTTTGAGGCGGTTGC AGGCGAGGCCCTTAGGTCCGTATTTAATGTTTGCTTTGTAGAAAAAGTCGC
				CCATGAGCAAACAGCATGTTTCTACTCTGTGATGTTGTTAGGGGGGCATGTATATCTGTATTCTT TTTTATTCTCTCCAAAAGAAATTTCATTATGCAAAACATTATCAGGCAATGCAAACTTCCACAAAATTCCAGGAAAAAAAA
WI-1729	172 A			TGTTGGAGAAAAGAGAGCTTCTCTCCCACCATCACCTGTGTTTTT GATGTATGTGTCCTTCCGTGGTTCTTCTCTCCCACCATCACCTGTGTTTTT
1		1		TGCCTTACTTCATTCCCACCATTACATTTGTAAATTGGAACTTCTAGGAGGT TAGAAGGATTTCATTCATTTCAAAAAAAAAA
				CTGCCGCTGTTGTAGTAACTGTGAGTGATGGGTGCATCAGTATAATCCTGAGCCTCCCAAGGTACAGC
WI-1732b 122 T C	122 1 0		-	TGCCTTACTTCTTGTTCATTCCCACCATTACATTTGTAAATTGGAACTTCTAGGAGGTTAGAAGGA
				TATGCTGATCAAAAAAGGGGACATATTCAAGAAGTNUCCCTGGGTTCAAGTATACTCCTGAGCCTCCCAAGGTACAGC
WI-1732	114 C T			CTTTCACTACTATTCATCATATTGGCTAAGGTATTCATCATATTGGCTAAG
1				GCGAATTTAATGACTCCAAAGGTAGTAATTCCTTTCCCCCAAAAAGGGTTTAATGATTGCGGCCAAAAAGGGTCAG CATAATGTTTGAATTTGCAGTTCACCTTGGJAGJTTTAAGGTGTGCTGTTTTTTGGCAAAAAGAGTCAG
				TGGGAGTGTCCGGGAAAAGGGCTAAAGTCTTGTAGTCAGACAAACCGGCTTGCAGTGGGGGTGTCCCAAATCAGTTTATGATCTCCAGCAGGTTCTTCCA
WI-1750	97 A G		: : : :1	GGTACACAAAGAAATGCTTGTGGAAATCTAC/A/GJTAGCGCCTTAACATTTTGGCTGAGTATTAC
				TGTACATGTGTAATGTGAACCACCATGAAGCTGGGCAAAGAACAATTCCTAGGAAAGTGTCATGTGCATCCATC
WI-1780	31 A G			ACTEGAGAGACCTTGTTGAGTACAGAGGACATTCAAGAATAATCATAAAAAAI
	<u> </u>	!		CCACTCAGTAATAATAGTGTTGGAGATAAGTATATGGTAGGCACA I AAI AAI IAI I I I CAGGCACACA CCATTATGATAAGAGTAGGGTAGAGCATCACACTTGGGAGACATATCTGGAGTAAGAGTAGAGTAGAGAGAG
				GGTGCTATTTCAATATCTACTAAGCATGACTTCTAGAAAATTACTTATTACTCTTGTCCTCAA GGTGCTAATTTCAATATATATATTATTGAGGAAAATAACTGGAATCA
WI-1803c	77 AG			GGAAAIGGGAAIACCIAIAAIACAGICIIAIIC

WI-1803b	77 A	: 			CCACTCAGTAATAATAGTGTTGGAGATAAGTATAGGTAGG
WI-1837b	112 CT	! 	•		AGGCTGATAGCAGGGGAAGGCAAACAACCCCAAAGAGCCTGAGTGAATTTGAGCT AAGGTTTTTTCATTGGGGAAGGTTTTAGCTTTCTGGGGCT CGTGAACAACTGGGAAGGTGTGGGGAACGTTTTAGCTTTCTGGGGCT TTTACTTGGGATTTTTCATAGCTGATCATAATTTAGCCATTTGATCACTTCTTTTTTCCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAATAGA
WI-1837	112 CT	<u> </u>			AAGGITITITITITATI GCACCIGA IGCCAAAACAAAACCI CAAAACCI CAACACA CAACACACAC
WI-1840b	79 GT	L		; 	ATTITATCTCCAGAGTGTTTTGAATTTACTAAAAGTTCCTAAAGAGCACCCAGAGCACCAGAGATCTTTCCCAGAGCTCAGAAAATGTAGCTTCATTAAGACACCTCAGACCTTGTTTAGGATCTTTAGTTTATCTCCAAAAGTTCCTAAAAGATCCTAAAAAGTTCCTAAAAGATCCTAAAAAGATCCTAAAAAGATCCTAAAAAGATCCTAAAAAGATCCTAAAAAAGATCCTAAAAAAGATCCTAAAAAAGATCCTAAAAAAGATCCTAAAAAAGATCCTAAAAAAGATCCTAAAAAAGATCCTAAAAAAGATCTCCAAAAAAAA
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			TOTALCAGACACCAGGACTAGICTIGICIGCATAATGGAATAATCAACTGGACAACCCCNG
			CTNAGGTAGGNTACCTNGGCAATTAGCCCATCTTACAGCTGCAAAAGAGGCTTGCTCTGAGAGGT
			AAAGTGCCCCAACGCCCAACACTAGAGAGCAGCCAAACAGGTGTTTGAACCCAGCTCTGCCT
			GACTTCAGATCTGTGTGTAACTGCCATGAGAAACCACTTTTCTTTGCTCC
0061) 	-	ATTCCACTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGGCACAGGATGCACAGCT
			ATTENCTICAGGATCTCTGGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTCAGAGTCAAGC
			AGCAAGCCAATGGGTAGGGAAAGACCAGCCICTJCTCTGAANCTGGGTCCCACGTGGAGATAGTGAA
10430	T ()		TACAGGGCACCGNTGAGCATTCCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943C	2		ATTICACTITICACAGIGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGGACAGGGATGCACAGCGT
			GTTGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTCAGAGTCAAGC
		-	AGGAAGCCAATGGGTAGGGAAAGACCAGCCCCTCTCTGAANCTGGGTCCCACGTGGAGATAGTGAA
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00 00 10461-1M	5		ATTOCAGETTCACAGEGACACAGAGTCAGATTAGGGCTAAGTTGGGGGGACAGGATGCACAGCGT
			ATTICCATOR GOAL OF THE CASE OF
			GI I GOGIAN COCANA COCANA A A A A A A A A A A A A A A A A A A
_			AGCAAGCCAATGGGTAGCAAAACAAAAGAAGAAGAAGAGGGGGGGTAT
WI-1943	164 CT		TACAGGGCALCGNIGAGALICAMANICACIOCAMAGGGCALCGNIGAGGGCALCGNIGAGGGCALCGNIGAGGGCALCGNIGAGGGCALCGNIGAGGGCALCGNIGAGGGCALCGNIGAGGGCALCGNIGAGGGCALCGNIGAGGGCALCGNIGAGGGCALCGNIGAGGGCALCGNIGAGGGCALCGNIGAGGGCALCGNIGAGGGCALCGNIGAGGGCALCGNIGAGGGCALCGNIGAGGGCALCGNIGAGGGCALCGNIGAGGGCALCGNIGAGGGCALCGNIGAGGGCALCGNIGAGGGCALCGNIGAGGGCALCGNIGAGGGCALCGNIGAGGGCALCGNIGAGGGCALCGNIGAGGGCALCGNIGAGGGCALCGNIGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
	-		CCAGGTGAGGCTGAAAGAAGGAAGGAGGCAATTGCTGTTGGAGTGAGGAGATTCTGGAGAAAACCCC
			GCAGAGCTTCATTCTGTTTTCAAAAGTGTGCCATGCANGGTCNTCTGGGTTGTGAGCTCTTGCCA
			TTATCACAGCTCCTGATGACAGATCATGAAAATAGGTACTTCCCAAGCTCTGACTAGACTTGACA
T 4 050 270 4 TM	270 A T	:	GTTGCAATTAAATCCGTGGTGTCTGAAAACTTAAAAATGCACCTCCCAACTT
20061-144			CCAGGTGAGGCTGAAAGAAGGAAGGAGGCAATTGCTGTTGGAGTGAGGGATTCTGGAGAAGCACCCT
			GCAGAGCTTCATTCTGTTTTCAAAAGTGTGCCATGCANGGTCNTCTGGGTTGTGAGCTCAINGCLGAA
			TTATCACAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGGCTCTGACTAGACTTGGCA
40000	270 A T	_ !	GTTGCAATTAAATCCGTGGTGTCTGAAAACTTAAAAATGCACCTCCCAACIII
MI-13000			CTGATGCCAAGTGCAGCTTAGAGTNAGGAATCCAGAGAAAGTNTTTGGATCTGGTAAGTAGGAGTCA
			TTCTGGGCATTTCTTCATAGAGTNTTGTTTTTAGTCTCGTAATAAIACIGIIGCCCIAGGAAAGAIIGII
			TTTCCTACTGCGTCTGTGAAAGCCTTTCCCCATCGAGTGATACAGTACTTICCAGTTACAGTTCCAGTACTTTCCAGTACTTTCCAGTACTTTCCAGTACTTTCCAGTACTTTCCAGTACTTTCCAGTACTTTCCAGTACTTTCCAGTACTTTCCAGTACTTTCCAGTACTTTTCCAGTACTTTTCCAGTACTTTCCAGTACTTTTCCAGTACTTTTCCAGTACTTTTCCAGTACTTTCCAGTACTTTTCCAGTACAGTACTTTCCAGTACTTTCCAGTACTTTTCCAGTACTTTTCCAGTACTTTCCAGTACTTTTCCAGTACTTTTCCAGTACTTTTCCAGTACTTTCCAGTACTTTTCCAGTACTTTCCAGTACTTTCCAGTACTTTCCAGTACTTTCCAGTACTTTCCAGTACTTTCCAGTACTTTCCAGTACTTTCCAGTACTTTCCAGTACTTTCCAGTACTTTCCAGTACTTTCCAGTACTTTCCAGTACTTCCAGTACTTTCCAGTACTTCCAGTACTTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCCAGTACTTCAGTACTTCCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTTCAGTACTACTACTACTACTACTACTACTACTACTACTACTACT
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			AAATTCTAGAAGCCAGAAGTCAGGTCACGATTTATAAAGTTGAAGTAAATGCATTGTAGTTGTAGTT
_			TTTCTCTTAATTCTGCACAAAACTAGCTAAAAATCTTCTTAAATCAGTTACTACTACTACTACTACTACTACTACTACTACTACTAC
			GGGTTAATGTAAGCACTCAAAAGTTATGTAGAGTAGCIGICICIGAAGICACIIIIICIACICICICA
WI-2012	WI-2012 102 TC	:	GECTTCACCAATGCTTCCACTGGATC

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			CTTTTAGAGGTGGTCATTTGGGTTCCCTTCGGAAAGTGATTCGTGTTTAAATGCTGATAATGCTGATACTGACACTTCTCA
			CCAGAAAAGAGAAATACCCATCATGAGGAAGAGAAATGACTTTTGTTCAGTTATGCTCCCGGGTCC
WI-2013 1	127 CT		CCTTTCACTGGAGGGATATCTCAGCTTTCTGAGCCCCTGGTTACTGCAATOC
			ACCAGACATCCCATCAGGAGTTAGTCCTTCTGGCAAGCCAGCC
			TCAATTTTTTCTTNACTTACTCATATATTGCTAGGATATCCACATAACCAAAAGCCAAACCIAACC
		- p	ACATCACCCAACTGGTTTTCTAGATGTACACGAATGTGGGGACCTCTGTCTCAACCTCCGACCTCCGACCTCTAGAAAAAAAA
WI-2032c 166 GA	66 GA	:	AGATCATTGGTTAGGCTCACCTTCCTGTAALTGCTTCTGTTTTTCAAAGGG
			ACCAGACATOCCATCAGGAGTTAGTCCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAACC
			TCAATTTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAAACC
	-		ACATCACCCAACTGGTTTTCTAGATGTACACGTGTGGGACCTCTGTCTCAACCTCCGACTTICACAGA
WI-2032b 219 CG	19 CG	•	TCATTGGTTAGGCTCACGCTTCCTGTATTGCTTCTGTTTTCAAAGGG
			ACCAGACATOCCATCAGGAGTTAGTOCTTCTGGCAAGCCAGCCCTGCCCT
			TCAATTTTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAAACCTAACC
-	-		ACATCACCCAACTGGTTTTCTAGATGTACACGTGTGGGACCTCTGTCTCAACCTCCGACTTTCACAGA
WI-2032 12	219 C G	:	TCATTGGTTAGGCTCA[C/G]CTTCCTGTATTGCTTCTGTTTTTCAAAGGG
	· 		CGTTTTCTTCTACATCTTGGGGNACATAAAGANGAAAGAAGNAGCTGTCTTTTTGTGGTAGTTTTGCT
			CAGAGCTGCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAAATACCTTACAGACTTAGGATTTGGA
			TTTTCATGGTGGTTGGCACAGCCCAGGCTCAACAGAACTAATACCTGCTGTTCJCATTCTGCTTCCAC
WI-2054b 188 CT	188 CT	:	CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGTCTTT
			CGTTTTCTTCTACATCTTGGGGNACATAAAGANGAAAGAAGNAGCTGTCTTTTGTGGTAGTTTTGCT
			CAGAGCTGCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAAATACCTTACAGACTTAGGATTTGGA
			TTTTCATGGTGGTTGGCACAGCCCAGGCTCAACAGAACTAATACCTGC[T/C]GTTCCTCTGCCTCCAC
WI-2054	183 T C	;	CAGOCCTATCTCTTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGTCTTT
	!		TGGGATTAAAACCCTGTTTTCTTCCTTCCCAGTTCAGTGTGCCTTAATGTTTGTGCTAGAAATTAACA
			TTAACAGCAGTAAAAATAGCTCTTAAAATGCACTTGCCGTTCACAAGGTGTTTCCGTGCTT[T/C]TGA
	-		TATCATCTGATCTTCCCAACCAGGGCTTATTTATGCCTAGGTAAGGGGTAAGCAAACAGAGGCTGTGT
WI-2573d	129 T C	:	GAAGTGAAATGATTTGCTTGCACAAGGTCATATGGCTGGGCTTGGACGAG
			TGGGATTAAAACCCTGTTTTCTTCCTTCCCAGTTCAGTGTGCCTTAATGTTTGTGCTAGAAATTAACA
		•	TTAACAGCAGTAAAAATAGCTCTTAAAATGCACTTGCCGTTCACAAGGTGTTTCCGTGCTTTTGATAT
			CATCTGATCTTCCCAACCAGGGCTTATTTJACJTGCCTAGGTAAGGGGTAAGCAAACAGAGGCTGTG
WI-2573c	WI-2573c 165 A C	:	TGAAGTGAAATGATTTGCTTGCACAAGGTCATATGGCTGGGCTTGGACGAG

				TARGET AGA TITAGE
	_			TGGGATTAAAACCCTGTTTTCTTCCTTCCCAGTICAGTGTGCCTTAAAGGTGTTTCCGTGCTTTTCJTGA
				TTAACAGCAGTAAAAATAGCCTCTTAAATTATGCCTAGGTAAGGGGTAAGCAAACAGAGGCTGTGT
	(CAAGTGAAATGATTGCTTGCACAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573d 129 T	5		:	CONTRACT CON
				TGGGATTAAAACCCIGITITCITCAAAATGCACTTGCGTTCACAAGGTGTTTCCGTGCTTTGATAT
			. ;	TGAAGTGAAATGATTTGCTTGCACAAGGTCATATGGCTGGGCTTGGACGAG
WI-25/3C 103 M	2			TEGENTTANANCECTIGITITICITICETTCCTTCCAGTTCAGTGTCGCCTTANTGTTTGTCTAGAAATTAACA
				TTAACAGCAGTAAAAATAGCTCTTAAAATGCACTTGCCGTTCACAAGGTGTTTCCGTGCTTTTGATAT
				CATCTGATCTTCCCAACCAGGGCTTATTTACTTCCCTAGGTAAGGGGTAAGCAAACAGAGGCTGTU
- 40E30 mm	0.0		1	TGAAGTGAAATGATTTGCTTGCACAAGGTCATATGGCTGGGGCTTGGACGAG
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	_			TTAACAGCAGTAAAAATAGCTCTTAAAATGCACTTGCCGTTCACAAGGTGTTTCCGTGCTT[I/CJ1GA
				TATCATCTEGATCTTCCCAACCAGGGCTTATTATGCCTAGGTAAGGGGTAAGCAAACAGAGGCTG1G1
				GAAGTGAAATGATTTGCTTGCACAAGGTCATATGGCTGGGCTTGGACGAG
Wi-2573a	129 1 0	:		CACTTOATECTCATGAACAAGCATTTGTCTTAATTTACAGACATTAAGAACAAGCTTTCC(A/G)CTC
				CONCITION TO CACCTATCACCTCAACCTCTTCATCCACTTTAAAGAGGTTTCTTTAGGTCCTCTGCAT
				ATCATGGAAGCCAACTACTCTATTAACGCTTTCCCAATGATGCAGCCCAGTTCTGCATACAGTTIGTA
	- 00		<u>:</u>	CAGAAATGCTATATTATGGAAACAGCTGAAAATGAAATATCGATATAC
WI-2868D	5 - 5 -	-		CACTICATGCTCATGAACAAGCATTTGTCTTAATTTACAGACATTAAGAACAAGCTTTCC[AG]CTC
_				CCACTTCCCTCCCACTATCACCTCAACCTCTTCATCCACTTTAAAGAGGTTTCTTTAGGICCTCTGCACT
				ATCATEGAAGOCAACTACTCTATTAACGCTTTCCCAATGATGCAGCCCAGTTCIGCAIACAGIIIGIA
0000			_ :	CAGAAATGCTATATTATGGAAACAGCTGAAAATGAAATATCGATATAC
0097-IM				CATGCTGTGTAACCTCTGTGCTGCTTGCTGTCGGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC
_				TTCAAGGAGCTTCTCATCTCATTGAGGAGACAAGATGAACATCAGGAAAATGAACGAAC
				AGAAATGAATAGAGCCCCATTTTAAATTATATCACAGCTTTATGICCACIICCIGIICCACAICAC
407 90 TAN	131 T		1	TGGGCTTTTACAAAGGAGGGCTTT
00/07-144	-			CATGCTGTGTAACCTCTGTGCTGCTGTCGGGGAAATTAGAGCAAGGAATTGTATATAATGATTC
				TTCAAGGAGCTTCTCATCTCATTGAGGAGACAAGATGAACATCAGGAAATGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC
	_			AGAAATGAATAGAGCCCCATTTTAAATTATATCACAGCIIIAIGICCACIICAIICCIGIICO
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L			TTAGCACACATATCTGTTGTGGGACTTAACTGAGACAAGGCATAAAAAQT/AJCAGCACCTGGGGGCACCTGGGGGCACCTGGGGGCACCTGGGGGCACCTGGGGGAGGTGTTGAGTTGCTTGAGTTGCTTGGAGGGAG
WI-2954c 4	49 T A		CARC
			TTAGCACACATATCTGTTGTGGGACTTAACTGAGACAAGGCJAGJTAAAAATCAGCACCTGGGGCACCAGGGGCACTTTAAATCCTCATACCTACC
			CCTTGGAAAGACTCTATTCCCTGGGCAACCCCCTTGGTCTCTGGCCATCCAT
WI-2954b 4	41 A G		GAG
			TTAGCACACATATCTGTTGTGGGGACTTAACTGAGACAA(GTJGCATAAAAAATCAGCACCTGGGGGCAA
			CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCAT
WI-2954a	38 GT		GAG
<u> </u>			ATTACAAATCCTACCTAGCAACTGCTGACACTTCOCAGTTAGACTCACCAGCATTCTAAGAGTAAC
			CTGCCAGCACCAATAAGCTTTCTTTCAAACAATTTGTGTAACCTCCTCCTCCTTCTTAACCTTTCTTT
			ATTICCTTTGTTCCCCTGACATTCTGAAGGCCACGCTGGTCTAGATGTGTCCCAGATIGCAAATCCT
WI-2971b	62 T C		AGTICTITAATGTTATTCTGAAAGAAAACCTTTTACTTAGGGAITIGICI
			ATTACAAATCCTACCTAGCAACTGCTGACACTTCCCAGTTAGACTCACCAGCATTTCTAAGA[T/C]G
			CTGCCAGCACCAATAAGCTTTCTTTCAAAACAATTTGTGTAACCTCCTCCTTCCT
			ATTTCCTTTGTTCCCCTGACATTCTGAAGGCCACGCTGGTCTAGATGTATGT
WI-2971	62 T C		AGTTCTTTAATGTTATTCTGAAAGAAAACCTTTTTACTTAGGGATTTGTCT
<u>-</u>			TTCCTGGGAAAGAAAGATGGGGGTTTTTNTTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC
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			AATCTTTCTTCTGGT[G/C]TTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG
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				TICCAGTTTTNATCAGGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGG
				AATCTTTCTTGGT[GCJTTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG
WI-2995c	151 GC	:		AATGAGACAGAACTAGCAGAAAGTGTT
				TTCCTGGGAAAGAAAAGATGGGGGTTTTINTTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC
				TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGG
				MAAATCTTTCTTCTTCTGGGGTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCTCT
WI-2995d	133 A T	:	:	GAATGAGACAGAACTAGCAGAAAGIGII
				TTCCTGGGAAAGAAAGATGGGGGTTTTNTTGTTCTCTGACTACAAICCAGAGALAACAICITTGCC
				TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGG
				AATCTTTCTTTCTGGT[G/CJTTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAAGGAAAAAAAA
WI.2995c 151 GC	151 GC		1	AATGAGACAGAACTAGCAGAAAGTGTT
2000				TECCTAGGAAAGAAGATGGGGGTTTTINTTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC
				TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGG
				AATCHTICTTICTGGTIG/CITTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG
			ļ	AATGAGACAGAACTAGCAGAAAGTGTT
O C DCREZ-IM	5 5			TTOTTEGGAAAAAAAAAAAAAGATGGGGGTTTTTNTTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC
				TOCACTITINATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGG
				MANATOTTTCTTCTGGTGTTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAA
				GAATGAGACAGAACTAGCAGAAAGTGTT
Wi-2995a 133.A I	133.4			CENTERAL CONTROL OF THE ACTION
	_			GIGGIGGAGIICALICATION OF TATOCT GITTLE TRATECT AT TO THE TATOCT AT TO THE
				AICICACITACO CON ICA
			_	GAALGAAL HACKI COOLONG
WI-3147	32			ATTOTATATTATTATCATTACTTCCAGTAAAATTCTTTATTGAGGTCCATGTCCATTACCTCTACTTAC
			· - -	TICICACAAAGAAGAACAACAACAAAAAAGCCTCTGTTTGCAATCTGGCCTCTTATAAATACTTTCTG
				TATATTTTAAACAAGTACTGTAGAGTNATGAATCATTACATCCTTAATAAGCATATCAAAATTTTAC
47000	- a	;	_!	TCAGTAATTCAGAAGGACAATGGAATGTACTTATTTNATATCTTAT
WI-9294D	01		:	ATTOTGTAATGTTTTCACTGCTTCCAGTAAAATTCTTTATTGAGGTCCATGTCCATTACCTCTACTTA
				TICIGACAAGCAAGAACAACAACAAGAAAAAGCCTCTGTTTGCAATCTGGCCTCTTATAAATACTTCTG
_				TATATTTTAAACAAGTACTGTAGAGTNATGAATCATTACATCCTTAATAAGCATATCAAAATTTAA
7000	5 P	- :	<u>:</u>	TCAGTAATTCAGAAGGACAATGGAATGTACTTATTTNATATCTTAT

WI-3564 177 C 1 AL	AGIGICACACATGCTTCCTTCACACACA
	TGGGACTTCACTGGTTGACTAACGTTAACATGCTGTTCTGTTCTAACAAGTGTTTGTGGTGTGTCATC
<u>8</u>	GAAAATCAATGTGTCTTCCCAGTGTATTCACATGGCACAGTGTCACAGAGGGCTTGAGCGTCTGAGCG
35	GCTAGTAAGGTTCCACCTAAATGGTTCCAAGTCAGGAGTCACTAAATGTTTTGAGAAATAAAAGT
WI-3564b 177 C T AG	AGTGTCACACATGCTTCCTTCACAAACAAA
21	TEGGACTICACTGGTTGACTAACGTTAACATGCATGTCTGTTJC/JAACAAGTGTTTGTGGTGTCATC
	GAAAATCAATGTGTGTTTCCCAGTGTATTCACATGGCACAGTGTCACAGAGGGCTTGAGCGTCTGAGCG
25	GCTAGTAGGTTCCACCTAAATGGTTCCAAGTCAGGAGGTCACTAAATGTTTTGAGAAATAAAAGT
131 GA GT	GTTTAATTGGGAAATATGTTTGCATAT
	AGGTGATTCCTTATGGGAAAATATATACAGCAAGAAAAAANANGGAAAAAATGTTGATGATACCT
79	GAAAAATTGCCATTTTTAATATCTTTGGAACTTCCTAACACATTACCTATTTTTNAACCAAAC[G/A]
	TAACTTATGCCTCATCTGGCTTACTGCTTAGTTCCCATTTGTCATCAGTGCACTTAAAAAATTATTT
WI-3505b 131 GA GT	GTTTAATTGGGAAATATGTTTGCATAT
	AGGTGATTCCTTATGGGAAAATATATACAGCAAGAAAAAAANANGGAAAAAATGTTGATGATACCT
	GAAAAATTGCCATTTTTAATATCTTTGGAACTTCCTAACACATTACCTATTTTTNAACCAAAC(GA)
	TAACITATSOCICATCTGGCTTACTGCTTAGTTCCCATTTGTCATCAGTGCACTTAAAAAATATTT
194 GA	ATCTCTGGNAGAAGCCACTGGGAAGTCGAAGGAGTGACTTCAAATCAGG
	CTGGAATTGGGATGAATCTNACATTCAATGTGCACCCTTCGTGTGGGATCACTTCTCC(GVAJTGCCCC
TA T	TAGCACGIGGCATTGIAATGGCTGGATTTCCTCCGCTCTAAGACACACCTTTATGCTTTCNAAGCTTT
33	CCATGAAGAATGAGTTCCTCCCTCCCTGGGTCACGTCTAAGAATAGCACACCCTTGAGAATTTNACT
19 G C AC	ACTGTGGATCAATTTATATTACTTTTGGATCAGTTTAGATGACTTTNAGTTG
*	AAAAAAATCATCAAAAAGTCGAAGTTAGTTTTNATTACCTTCACCTTTTCAATGGAAAACTTTATAA
5	CTTTTAAAATATGATTTCTTGAAGTGGCTGCATACTATTCCTTCC
	CCATGAACCATGGGCTACAGCJATATTCCTAAACTTCAGAGTCCCTCCTTACTGGAGAGGGATCCA
106 GA GA	GACACAATGGAAAAATGGAAAACATTCATGGAAAAAAACCCATTTCAATC
	GCCATGAATATTTTCCATTGTTTCTCATTAATGTATTAATTA
	TOCCTGTCCCCGTCCCAAGCCTATGTTACTGGTATGCTJG/AJTGGTATTGGATTGGATGGATTACTT
	GTTTTGCTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACTCATCC
WI-3292b 106 G A GA	GACACAATGGAAAAATGGAAAAACATTCATGGAAAAAAACCCATTTCAATC
<u>8</u>	GCCATGAATATTTCCATTGTTTCTCATTAATGTATTAATTA
5	TOCCTGTCCCCGTCCCAAGCCTATGTTACTGGTATGCJJQAJTGGTATTGGATTGGATGGATTACTT
	GITTIGCTAGACTAGGAGTITICAGCITICATCCAAATCCCTITAAGGATANITAGCTCTGCACTCATCC

0796				AATGICCATGCTGTGACTGACCTGTCTAACACCTTTCCTAGTATTCCTTTAGTGGAAGATTCAGAGGGGAGAGGGAGG
6400°-14	5			ACAGTACACATGGCCCCATTATGGAAACAATCATGTGACTTATGTTACTGAGAAGTTCCCTCTAA ATTTAACTACCAGGCGGAGTGCTTTTATAGTAATTAAAATATGTTTAGTAAATAGAAAATG /cjaagaaaaaatgatgagtcaagttgtagacactatttaaaattgtaacttggtcaaatgattgtt
WI-3674b 133 GC	133	 O		AATTCTTAATTAATTGTTTTATGTTTTNATTACTGCCAATCACAGCCAAG
-,				ACAGTACACATGGCCCCATTATGGAAACAATCATCTGACTTATGTTACCTGAGAAGTTCCTCTGAAATTAACTACCAGGCGGAGTGCTTTTATAGTAATTAAATATTATTATATTAACTACCAGGCGGAGTGCTTTTATAGTAATTAAAAATGTTTATTTA
WI-3674	133 GC	 GC		AATTCTTAATTAATTGTGTTTTATGTTTTNATTACTGCCAATCACAGCCAAG
				CAATATAGACCAAATGACTGCCACAAAGAGAAATTAGTGGATCTACATTTAGAAACCACATGITTTT ATTGGCTCTTCTCTTTCTCTCTCTTTTTAATGCTCTCTCCCAACACCAATTCACTTTATTCTTTTCAA T(G/A]AGCATTTGTCCAATTTAAAGTCAATGAAAAATAATGTACATTTTCAACAAGTATAAA
WI-3682	137 G A	<u>ਂ</u> ਰ	:	GCCCTGCAAAAGIGCI I ALALGA MI GGTATGTTGAGGTCAGCTAATGGTCACTGTGGGTTTGGAGTGAATCTAAATGGATTTTTTTGCCCTTGGA GGTATGTTGAGGTCAGCTAATGGACTTCTGCATGGGCTTAACTCTAACTTAAGACTTCTTAATTAA
4	Š	- 0	ļ	CAAAGACCAAGGAAGGAATTATGACCACTTTACAACTGAGGAAATCAAAGCAAGGAAJAGAA GTTAAATGGCCTGTCCCACTCCACAGAAATGGTTATAACAGAGTCAGAGCCA
0+000-IA	7			GGTATGTTGAGGTCAGGTAATGGTCACTGTGGTTTGGAGTGAATCTAAATGGATTTTTTGCCCTTGGA
				CAAAGACCAAGGACAACTGTAGGACTTCTGCATGGTCTACCTCACTTAGGCTTCTTGATTAATAACTC
WI-3854	194	¥	i	GTTAAATGGCCTGTCCCACACAGAAATGGTTATAACAGAGTCAGAGCCA
1				AGCCAGCCACATCATGTTGAGTCCTGCTCATTCTTCCATCTTATTTTCTCTGTACTGCCTTCACCTTCCCATTAACAAGAACTCTTGTGATTACATTGTATTGTGGTTACACTACAGAATCCAAGATGACTC
WI.4039	200	<u>ه</u>	1	CCCATCTCAAGGTCAACTAATTAACACCTTAATTCTATTTGCAATCTTTGTCATTGTCATTACCATAACATATT CATGGGATTTCTGGGATAAGGGGTAGACATTTTTATGGGAGGCATTA
1				GAAAAATGATGTTTTTGATTTCCCTTCCTATCTTCAGATTATTGGAGTGTCATTAGAAAACTGATAGT
				AACCTTTATTTGATGAAACTCTGTCTATAATTAAACCTTCCTCTTCCTGCTTTATTTGAGTACAGTACAGTAAAAAGTAGCAACCATGGG
1000	130	: 	, i	GTAGGGACAAGTINCAGAAAAAGGGAAGGTINGGGGGGTTTTCTGGGAAGA

			GAAAAATGATGTTTTGATTTCCCTTCCTATCTTCAGATTATTGGAGTGTCATTAGAAAACTGATAGTAGAAAACTGATAGATA
WI-4110	130 T C	•	GTTTAGGTAAATAAAAGTGCCCAAGAATTCAGTATTCAAGTACAGTAAAAAGTAGCAACCATGG GTAGGGACAAGTNCAGAAAAAGGGAGGAGGTNGGGGGGTTTTCTGGGAAGA
			ACCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTTGGGTGGG
Wi-4119b 168 GA	168 GA		AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA(GA)CAAGGTACCAAATTTGTTTTCTTTCA TGAGACCGTCTGCATTCTTTTGTTTTTTAAAGGGCTCTGTTGATCATCATCATCTCA
			ACCTCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGGGCTTGGGTGGG
WI-4119	168 G A		AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA(GA)CAAGGTACCAAATTTGTTTTCTTTCA TGAGACCGTCTGCATTCTTTTGTTTTTTAAAGGGCTCTGTTGATCATCATCATCTTCA
			CAAAGTCAGATTTTGATTATCAGGATAACAATTTTGAAAATAGAAAAGTGT/GJTTTAAACTATTT CAAATAAACAATAAAGAAAAACATGATGATGAAATTCTTCGTTACATAATTGTATAGAATTTAGTGGGG
WI-4123b	51 T G	!	TTCTTCCATGACATTGGCTTGTTCTTTCTCTCAACAGTGGGTGG
			CAAAGTCAGATTTTGATTATTCAGGATAACAATTTTGAAAATAGAAAAGTGT/GJTTTAAACTATTT CAAATAAACAATAAAGAAAAACATGATGAAATTCTTCGTTACATAATTGTATAGAATTTAGTGGGG
WI-4123	51 T G		TTCTTCCATGACATTGGCTTGTTCTTTCTCTCAACAGTGGGTGG
			TIGIACATGITICATICATCCCCCCCCATTCTTTTCTGTCTTATAAAGAACCTCGCTTCTTCCAAAGTTCTTCTCAAAGCTTCTCAACTTCAAAGCTTTCTATATATA
WI-4149b	145 GC	:	GTGCTGT[GC]CCTTGTGAAGAAGCCAGAGCCGAGCATACCAACATGATCTTTTGCTTGAACTGTAGT AGGAGAGACAAGACA
		•	TIGTACATGTTCATTCATCCCCCCCCATTCTTTTCTGTCTTATAAAGAACCTCGCTTCTTCTCTCCCAAGT
H 100	——————————————————————————————————————		CHACHCICCACCHAGCCACACAHLICHINI I ICCAICANAGCH I CICAGCATCATTTGCTTGAACCAGAGCCAGAGCAGAGCAG
8011			TAACACACHTICATTICGTTTCCTATTACTGCAGTTAAAGGAACCATCCATTACAATTCCCTC
			AGITCIATECTITAGAGINCTATTATAGGACTACTGTAAAATTTCAGAGGGAATTACTCCTTGGAGTA
			GGGGAATGAGTTAAATAATCTACCACATGCCAATTGCAGGGACTGTGGTTAA(GAJATGTCCTCTCT
WI-4182	WI-4182 188 GA		TGCCCCTTCCCAAGITCTTAAATICCTAG

				AGAGACGTTGAATGGGGACATCTTTCTATTTCGATTTTAGTTTAACATTTGATAAGAATTGATGAAAAAAAA
WI-4230	 	1	:	TTTCCATGGTAAAAAGAAGTTAGAGAAAAACAGCCTATTTTCTTAATGTTAAATGTAATTCTGAATGAA
-	ļ			GAAAATTOCATTGAAGTTTTGACCTTGAACTGATCTCATTAAATTCTCTCTC
				TAGCACTGTTAGCACCAGAAACTGTGAAATTATCTCCTAGATATTCTTCAGAATCTAGGATGGAAG
WI-4241 1	118CT			AA
				CAGGGCTTTTTGGGAAGATCAGTTAAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTCAGCAT
				CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAAGATCAAATAAGAGCUTAGG
W. 42715	- C		:	GGACTGAATCCAACGGGGAATATTAGAGTNCTACAGGGAGGCCCCCAACCCTCCCCCTTTGCGCCCCCCCAACCCTCAGGAGGTCCAGGTCAGGGAGCCC
21/2				CARRECTITITINGSAAGATCAGTTAAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTCAGCAT
				CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAAGATCAAATAAGAGCCTCAGG
				GGACTGAATCCAACGGGGAATATTAGAGTNCTACAGGGAGCCCCCAACCCTCCCCCTTTGTCTCAGG
WI-4271	151 A	:	:	CTCTTAGAAGGTCCAGTCAGGGGC
	:			AATCGAAACATTGATTTTTTTTTGTAAAGGAACCACATTATTTAT
				GAAATTTGAAAGGGATGAACCTGGAGGAAGAAGAATAGAAAGGATATTATTGCATAACCTTTGGA
	_			AGGTAAGATGTGAACCTATACA[G/A]TNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA
WI-4389b 156 GA	56 G A		:	AGAGGTATTGTAGGAACTGGAAGCGGTAA
	1			AATCGAAACATTGATTTTTTTTTTAAAGGAACCACATTATTATGATATTTGTGCCCAGTTTAGCATAT
				GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAATAGAAAGGATATTATTGCATAACCTTTGGA
				AGGTAAGATGTGAACCTATACA(G/AJTNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA
WI-4389 156 GA	56 G A	:	;	AGAGGTATTGTAGGAACTGGAAGCGGTAA
				GATGACAATTATTGTGTATTGGCATTTTAAA(A/G/GTACCATTCCATTTTCTTCTGGCTTTCGTGTTT
	_			TGTTGTTGAGAAGTCAGGGGTTAGTCGTATTGCTCCTTTTCTAGTTCTTCTCAGTAGGAAGACTGATC
				CTAAACAACCTAATTACCCATGCCAAGTACGTCCAAACTGATCTTTAAAGAACATAAATCAAATTG
WI-4488	31 A G		;	TATTATCCTATGCTTAAAATGCTCAG
				ACCATCAATGTATCACCTTCTAAAATTTATTAGATGATTAACTGGCTCTGTTAAAAAAATAAAAACCT
				GTCTTGGACATTGAAAATAAAACATTACTATTGGTCATTTTCTGCTACTTACAAAGGTACTGCACTA
	_			AACAAGTTAAGIG/CJGTTTTTTGGAGGGGAAAAATCATAAAAATGCATAAAATTTCTACCACTGTCA
WI-4491	145 GC			TITCTTGTCCCATAAAATTITACATGCCT

			_	
••				TTGGTTGGCATTTTAGCCTCATAACAACTATTTACAATGATTGTTACTCTTATTTACAAGGAGG AAAAATGAGGCTTAACATCACACTTCTGCTTAGTCGCAGAGGCCAAGATTGAAQCCAGGAATCCATT CACCGGTAC(WGJTGCTACCTGGGTAAAAAATGTTTAATTAAAATCTATGGCATTAGATTTCAAAGA
WI-4584	144 A G			GICCTAATGIGGITITGAAAATAGGIGGCTTTAATTTGTTTATCAGTATGC
				TTTCTGCATTTGAATGTGTATGGTCAGACTTCAGAGGAACCCAGGAATCTCATTTATTCAGTACAATTCCACTTTAC TGGTGGCCAGGTGCTCAGGCCCTATTATCAGAGAGATCTCAGTTTAACTTTCCAATTCCACTTTAC
WI-4639	185 CT	-		TGACCATATGACTTGGGGAACAȚTATCTCACCTATCTGAGTCTGTATCQC/JCATCTTAAATTGTA AATTTAAGGACACCTATCATAGTAATATTGTGAGGATAAAATGAAATAA
Î	<u>. </u>			
				AAATGAATCCGCTTTAGAGCAAATACCAGTAAGGGCTGGTGCAGGATGGTGGTGGCTGAGAGA/~
				JGATTACTCATAAAAGCATATTATAATTTTATAAATATGGAAAATTTAACTAGATAATTAAATGTGAAT
	_			TGAGTTTGAAGGTTGCATGAGAGTAGGGAGGAGGTAGTTTCTACTTATAGGGTTTATATAAGTNTGCT
WI-5327	63 A	•		TCAATAGAATGGCTCTTTCGGATGACAATGATGAACTGTTCTAAGCAGACAG
	:			GCTTTTGAGAATGAAAAGGGGAGCCTGGACCATTGCAGGGCTTCTTCATCTCTGATTATTTTGTGTAT
				TTATTGTTCACTTATTTAT[C/T]GTCTGTCTCCCCTTCTGGTATGCTTGTGTCATGAAACAA1GAATTC
				CCCAGTGCCTGGCCCGATTCGTGGCTCCTAGAGGTGTCCAGAAAAAAAGTTTCGGTGAATAGAATTG
WI-5390	87,CT	;		ACGAATGGGTTCAGAATTGAAACCTGTGAATCTATGGAAGACAAACGAAT
				CCTTGCCTGCTTTATGCATAATGAGAATAGAGTTGACTCTCCTGTCAAGAAATCAATTATTAAGCAGT
			_	GCAAACATTATTTTAATTT[G/AJAAAGAAACTTGTTTCTGAAACTTTGTACTCTTGTAGTNAAATTG
				AATCTTTCCTTCTCAGCAGTTTCCATGGTCGTGAATCCACCCATCTCTTTTCACCAGTAGCAAGATT
WI-5404b	87 GA	i		GCTACTTATATGGAAGGGTTTTAGAGTTCATAACAA
				CCTTGCCTGCTTTATGCATAATGAGAATAGAGTTGACTCTCCTGTCAAGAAATCAATTATTAAGCAGT
				GCAAACATTATTTTAATTT[@AJAAAGAAACTTGTTTCTGAAACTTTGTACTCTTGTAGTNAAATTG
				AATCTTTCCTTCTCAGCAGTTTCCATGGTCGTGAATCCACCCCATCTCTTTTCACCAGTAGCAAGATT
WI-5404	87 GA		<u>:</u>	GCTACTTATATGGAAGGGTTTTAGAGTTCATAACAA
				TAGGAAAGGGGATGGTGATGGCCTCTGAGACATTTAAATCTATTCTTTCACCACTCACACTGCCGCCA
				TATCTCCTC[A/C]CCAACACCTCTGTTTTCTGACAGCCAAGTTTCCATCAGTTGATATGGGACTATTT
				GTTGCAAAACAATTGTTAAAAGATTTGGCTGACTTTGGCTGAATTTGCTACAACTCCAAAAGANTC
WI-5545b	77 A C	;	•••	GAGATACACCATGAATTTTATTTTCA
				TAGGAAAGGGGATGGTGATGGCCTCTGAGACATTTAAATCTATTCTTTCACCACTCACACTGCCGCCA
				TATCTCCTC/A/C)CCAACACCTCTGTTTTCTGACAGCCAAGTTTCCATCAGTTGATATGGGACTATTT
	_		,	GTTGCAAAACAATTGTTAAAAGATTTGGCTGACTTTGGCTGAATTTGCTACAACTCCAAAAAGANTC
WI-5545	77 A'C	;	:	GAGATACACCATGAATTTTATTTTCATTTCA

			TOTAL
			ACTCAAGTTTGGGGGATAAAATCAGAAGTTTCTATGTAACCTAACTGAGGAACTACIA
-		·	TTCTTTTTTATATAAATTATGGATTIGIIIIIACIICCCIAACCAACCIICIAAGGGAATCA
			GJTTATACTGGAATCATGTGAAGACATTCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGAACCAAGGTACCCAGGTGCACATAGTTTTAAAGGGTACCCAGGTGCACATAGTGAAGGGAACAATAGAAGGGAAGGGAAGAGAGGAAGAGAAAGAA
WI-5860b 134 A G	<u>;</u>		ATTTCCAAATCATCACTTCTGTAT
	!		ACTCAAGTITGGGGGATAAAATCAGAAGTITCTATGTACAACTTAAATTTTGCTAAGATTITTATTGT
			TICTITITIATATAAATTATGGATTTGTTTTTACTTCCCTAACCAACCTTCTAACTGAGGAACTAC A
			GITTATACTGGAATCATGTGAAGACATTCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGAATCA
134 A G	<u>:</u>		ATTICCAAATCATCAACTICTGTAT
7	:	1	SCA & & CA & CA & CC A
			TATATATATICITATICITATITATITATITATATITAGAATCTGATGAGATTTAGCATGGGATAAGTGCAG
	-		TO A GAGA TA GAGA TA GAGA TOTAL TOTAL CANDER A GAGA GAGA GAGA GAGA GAGA GAGA GAGA
0			TAATTIC/GIATAGTAGGTCACCACAAAGTCTATATTGTATGTAGGAAAG
Wi-6106 208 C			CONTRACACATATECCAGACCAGACCAGACCAGACCTGTCATATTTCTGAGAGAATGTAC
			ATCACTETTOCTTCTTCTCTATATATATCACTCACTCGCTGGAATAAAACGAAAAAAAA
			A I I GAGAGA TOTAL CONTROLL TO THE ABANTATA TOTAL TANDERS AND TOTAL TOTA
			AAACCCIAIAIIINCIGICIIGIGAAAAAAAAAAAAAAAA
WI-6109d 129 T C	•		GNAAAAITATCCCCTGAAAAITTATACCA
			AAGATAGACAAACATATGCCAGACCAACAAAAACACAGACCTGTCATATTTCIGAGAGAAAIGIAA
			ATTGAGTCTTCCTTCTCTGGGACTATAAGGAGATCAGGTGGAAI AAAAUGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGA
			ACCCTATATTTNCTG[T/C]CTTGTGCATACTTTAAAATGTATATGTGGGAGGAAGGAAI I I I GA I Y
147 147	_;		TGNAAAATTATCCCCTGAAAATTTTATACCA
25010-100			AAGATAGACAAACATATGCCAGACCAACAAAAACACAGACCTGTCATATTTCTGAGAGAATGTAC
			ATTGAGTCTTCCTTCTGGGACTATAAGGAGATCAGGTGGAATAAAACGAAGGAAAAAAACCTAA
			ACCCIATATITINCTG[I/C]CTTGTGCATACTTTAAAATGTATAATGTGGGAGAGAAGGAATTTTGATG
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			TGNAAAATTATCCCCTGAAAATTTTATACCA
0 10 10 10 10 10 10 10 10 10 10 10 10 10			AAGATAGACAAACATATGCCAGACCAACAAAAACACAGACCTGTCATATTTCTGAGAGAAATGTAC
			ATTGAGTCTTCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAAACGAAGGAAAAAAAA
			AAACCCTATATTINCTGTCTTGTGCATACTTTAAAATGTATAATGTGGGGGGGG
W. 61002 129 T C	:		GNAAAATTATCCCCTGAAAATTTTATACCA
			AATGCCTATCACCTTCCATCATGCTGCATAACTGATTCATAATGCTTATTGTTTAGCACCTGTC
			TTCCAACACATGCTGTTTTGTTCAATGA(T/C)GCATATCCCCAAGTGCCTTAGACAATGCCTTAGACAATGCCTTAGAGG
			AGTGAACAGTATTTGACTAAAACATACTTGTTAAATCAATAAAALIAATCAACIGAACHIGGCALAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
WI 6112 96 T C		•	GAAC
•			

WI-6244	103 T C	ļ	TAATTGCACAACTTACATATCAGGGTTTCTGATTGAAAGGAAGG
: 			CTGGCCTTATATATCCAGGTTTAGGATTAATCTTACCCCAACTTAATAGACTTCCAGACAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTAGAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTGCAGTTAGAGTTGCAGTTAGAGTTAGAGTAGAGTTAGAGTAGAGTTGCAGTTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGAGTAGAGAGTAGAGAGTAGAGAGTAGAGAGTAGAGAGAGTAGAGAGAGTAGAGAGAGAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
WI-6268	124 CT	•	GGGTTCCAAAGATTTCGTTACGATTTTTA
			AGGIGCCATITAATCCATTCAAATTTGGAAGCTACATCTTCAAGGGTCTGAGAGAGCTCACTCCCCCCATATATTCCCCCTTTACATGTTTTCTTATAAGACATACAGTTTAATCAATTAACAAACTAAAAGAGCTTAATAACTGGCAATATACAGATGGGTTTATGTCAGAGTAATAGATGAACATGAAATGGACCATGTG
Wi-6336b 234	234 C 11	:	AGGTGCCATTAATCCATCAAATTGGAAGCTACATCTTCAAGGGTCTGAGGAGCTCACTCCCCCC
WI-6336	034 E		ATATATTCCCCTTTACATGTTTCTTATAAGACATACAGTTTAATCAATTAACAAACTAAACGCTTAATACTGGCAATATATTACAGATGGGTTTATGTCAGAGTAATAGACATGAAATGGACCATGTGGTAGAGAGTAATAGACAGTGAATAGACAGTGATGAGAGAGCATGTGTGTG
A Constitution of the Cons			TTGGATACAAAATTCAGTTACACAATCAGTAGCATTCAAAATTAGTTATGAGTATTTATACAATTA CAAAAATGGGNTTCATGTTTTAAAAGCACAATTAAAAAGCTCAAACATTTTAAAAACAGGCACAATAATCTAAAAGGCATATGAATGGGCTTTTGAAAGCTCCCCACCTTCACAATCAAAATC
WI-6381	92 CA		GGTTGAGGCATTGGGAAAGGCAGAAATTGAGGCAGTAGAAATTGGACATTTTAGGAAAAGAGAGT
WI-6436	198 C	i	ICAGANGACAAAGICA IGACAAAAAAAAAAAAAAAAAAAAAAAAA
			GAGGCCTCTTTGCTTTTCCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTTTGTTCTGATTGGTTGGTGCTCACACTGCCCAGATTGTTAAATATTTGAAAATC GTATCTGGTTCTATCATCTGCATCTCTGATCTTGTGTGGGCTCTATTGTTATCTATC
WI-6449	186 CT		TCTTATGTCAGACCTGAAGTTCCTCTAATTTTCTGTGGTGTATTATA
			GAGGCCTCTTTGCTTTTCCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATAŢGT GTATGGCTAGTGTTTGTTCTGATTGGTTGGTGCTCACACTGCCCAGATTGTTAAATATTTGAAAATC
WI-6449	WI-6449 186 CT		GTATCTGGTTCTATTCATCTGCATTCTCTGATCTTATGTCTGGCTCTATT[C/TJATCCCTATTCTCTGA TCTTATGTCAGACTGAAGTTCCTCTATTTTCTGTGGTGTATTTATA

				A A STITUTE OF A STORY
-				GCTGGAGAGAAAGACCTCCAAAAGAAGAAACIAAAICAGAGICICIIGAGAAAAAAAA
				AGAACA[T/C]TGAAAAAATTAAAGIAGAACICAAAGAGCCAAAAGICCAAAAGIT/C]TGAAAAAATTAAACITAAAGIAAAGAAAAAAAAAAAAAAA
				TAAGAAATATTTTGAATGGAAATCTTAAGAATGATTTTATTGATCAGTTAAAIGIICIICUUUUUU
WI-6463	72'T C		;	CAGTCCCATTTATATGACATTCCGCATGCTG
	-			AAGCAGTAAATCTTCCATCATGCCATGGATGCCAGTGGGTAAATGTTATAGAAACTTCAGAGGANAC
	~			AGAGGCAAAQCTJGTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC
				AAGAAAAGTAGGATTTTGAAAGGCACAGAGAAAAGGGGTGTACTAGAGGAGAACTATGTAAGCAG
WI-6474b	76 C T	•	:	AGGTATAGAGGAACTAAAAGTATAAAAGAGTGAGCCATAACTTAGGGTACCATAA
)		. •	AAGCAGTAAATCTTCCATCATGCCATGGATGCCAGTGGGTAAATGTTATAGAAACTTCAGAGGANAC
			•	AGAGGCAAAICMGTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC
				AAGAAAAGTAGGATTTTGAAAGGCACAGAGAAAAGGGGTGTACTAGAGGAGAACTATGTAAGCAG
1411 5474	7801		;	AGGTATAGAGGAACTAAAAGTATAAAAGAGTGAGCCATAACTTAGGGTACCATAA
775)		:	GAACTCAATTAACTTTGCAACACTGAGAAAATCGGATTTGGAGATCTGCAAAGCTGAGGTTGAGATT
				TRESACCTESTICAAATGGGGAATGCCACGCTTCGAGGCCTGTCTATATGCTTTATTTTGTGA
				CACTETCTATTTACCTCCCCCAATAGTGGAGAATCAGAGTIAJGCTCCTTGTCAGTGTTGCTACAGA
	+		;	GAAGATATACAGGATGGAAGGACAGCTCCTTAGGCCTAGACACACTG
W1-64/60				GAACTCAATTAACTTTGCAACACTGAGAAAATCGGATTTGGAGATCTGCAAAGCTGAGGTTGAGATT
				TTGGACCTTGGTGATCCAAATGGGGAATGCCACGCTTCGAGGCCTGTCTATATGTTGTGA
				CACTIGICIATITIACCTCCCCAATAGTGGAGAATCAGAGTIAJGCTCCTTGTCAGTGTTGCTACAGA
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WI-6564b	54 GA			GTTCCTTGGCAGGAGAACATGCATATGACTTTAAAATAAAGACCAACA
				TTCTTTATTGGTCCTACCAATGTGACTCTTTACCCAGGCCCACTGTTCCTATGCGACACTGGTTTG
				TAGGCATTCACATCATATGTCTGTGTCCTGAAAATCTCAATTAATT
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WI-6564	54 GA			GTTCCTTGGCAGGAGACATGCATATGACTI JAAAAI AAAGACCAACA

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				GTTAGACAGTATCCAGCAAAAAGGITATTTTACTCTGCATTCTGTCTTACTCTGTTGGTTTCATGTAAAATCACCATCAACTCAGCTGCAGGCATTCTGTCTTGGTTTCAGTTTCAGTTTCAGTTTCAGTTTCAGTTTCAGTTTCAGTTTCAGTTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAAAACTA
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				CAGAAATACTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAA GAAATTTGGGGAATTCTGAGGAATTCTGAGGAATTCTGAGGAATTCTGAATTCTGAAATTCTAAAAGGGAT
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				GCATTGCCATTCAGGGCCGGAGTCAGGGTTTGTGGGGCCAGAAGTTTAGAAGATT IGGGGAATTGTAAACACAGAATTGTAAACACAGAAATTGTAAACACAGAAATTGTAAACACAGAAATTGTAAACACAGAAATTGTAAACACAGAAATTGTAAACACAGAAATTGTAAACACAGAAATTGTAAACAAGAAATTGTAAACACAGAAATTGTAAACACAGAAATTGTAAACACAGAAATTGTAAACACAGAAATTGTAAACACAGAAATTGTAAACACAGAAATTGTAAACACAGAAATTGTAAACACAGAAATTGTAAACACAGAAATTGTAAACACAGAAATTGTAAACACAGAAATTGTAAACACAGAAATTGTAAACACAGAAATTGTAAACACAGAAATTGTAAACACAGAAATTGTAAACACAGAAATTGTAAACAGAAATTGTAAACACAGAAATTGTAAACACAGAAATTGTAAACACAGAAATTGTAAACACAGAAAGAA
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WI-6704c	33 T		:-	CAATGCAACATCCACCAATGTTTTAACTTCCACATATATAT
				TIIIGAAAAIAAAIICAIGAACAAACAAAAAAAAAAAAAA
				CTATTGCTCTTTAAATATGGTTGTACATGTCATCATTAATCGATTCATTGTTCTTCCACATGGTTAIT
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				ACATACATAAAATCAAAAATCATACCATATAAACGIIIACAAAIAAGIIIIICAIGACAAAAAAAAAA
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WI-6/93	2			CACAATAATAAAATCACTCCCTACCTTGAAAACTTTA(T/C)AGAAGCATTTTAATTTTACAACACA
	_			AAGCTCAAACGNACCTACAATAAGTCTAGTAGTCTGTTTACGNGCCAAGGGATAAGGCTGAACAAIA
				AATTAACCCTTTAAAAATGTCTATGNACAAGTACAATTTTCTTTTGAGTTCTGCAGAGCAATGACC
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00100-104	5			CACAATAATAAAAATCACTCCCTACCTTGAAAACTTTATICJAGAAGCATTTTTAATTTTACAACACA
				AAGCTCAAACGNACCTACAATAAGTCTAGTGTCTGTTTACGNGCCAAGGGAN AAGCTCAAACAN AAGCTCAAACGNACCTACAATAAGTCTAGTTTACGNGCCAAGGGAN AAGCTCAAATAACAA AAGCTCAAAACAAAAAAAAAAAA
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l .	- C			GCATGATTAAACCAGTGCAGAAAAATACCAAGTACATTGGGTGAACGATGAGCTAGCT
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				GATGGAAAGCCATTTTATTTTTCTCTAAATTTTAAAAGACACTTTAATGGAAAACATTTAGTAC CATCATGTCACCCTGAATGCCAGCAATACCTCGACTTTACACACGCAGGAAGCCTAGTAAAAGCCC
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WI-6826h	154 A			ATGCAAAACCTTGTACAT[AGGAGCTTAAATAATATCAAAATGCAAATATAGATTGGGTGCACTGT TAAGCTGAATTGCAAATTATGGCAACACACACTGGACTGGGGTATACGTTG
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WI-0840	5			AGTGCAAACTATTTTGAACAAAAGTAAACTATGAGTCACAGCATTCAGCAAGACATCAGACAGA
	- 5		1	TATTCATGCTTTTTCAATAGTCTCTTAGTCAACTTTCAGTGTAATTTCCACAAATATATAGCAGCTCA AACACAAATGCAGGAGCACAATGGCAAAGTTTGGCAACTGTTTTGGGCTAATT
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0000	T J & Z	; -		AAACACCATTCCACAATATTTGCATGCCCTAGTTGCCTATTTTATACATATC

				CACTCAAAACCTTTATTCATTGATTTACAAACTGTACAATATTTACAAAGTTTAGGCATTAATCCCA TATTGACATGAATGCTGTGGAGAGTCTAAAAATAAAAT
WI-6910b 163 GT	163 6		-	GGCTCTTTACACTTAAGCCATTACCAATA(G/TJTGAGATGTAATGGAGAATTTAATGTGGTAGAAAA GTCAGAGTGGCTGACCAGTCCCGGAOCTTCCATGTGAATGACTCTTGGC
	<u>.</u>			GCTIGITITITIGITIGITITITIAAGIGACACCTIGGCCTIGIGGGCATTICTICACTIAICTIACCCAAAAGITGCCTITIGGGCCCAGCCACTGACTGATTTAAAACCCAGAAAATGTGGTTTTAAACAATGTGGT
WI-6915	144		1	CGTGGTGAATTCAGGTGATTTTNATTTCTATTTGGTAGTTTTTCAGATTTCCCACAAAGAAGTG TATTGTCTTTGTAATTTGAAAAAAAATCAACAAGGATAGTAAAGATAT
1				CAATCAAAAAGTTCCAAGTTCAAAGCTGGGATGAAAAGCCAGGTCTTCTGACTTGCACTCTGTCCACACTGGATTTNCCTCTGATCCAGTCGCAGCCTCCCATAAGAAGTTCACTCTTAATTTCATGTCCATG
WI-6928b	175 T.C	;	i	CTTGICTTGGTCCCTGTGAGGAAAGGGGTCAGCTAAAGGT/CJAACTGTTCTATAAGGATGGGTAGG
				CAATCAAAAAGTTCCAAGTTGCAAAGCTGGGATGAAAAGCCAGGTCTTCTGGACTTGCACTCTGTACACTTGTCCATGACTTCACTTAATTTCATGTCCATG
				ACTGGATTTINCCICIGATCCAGCIBCAGCCCCCATAMACAGTICACTCTATAGGATGGGTAGG
WI-6928	175.10			THE ALGARACATTICAGATICOCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGA
	_			CTTTTATAGTAC(GA)NGTCATGTCCCAAATTCCCAATCCTAGGTAAGATATCAAGTTACAAANTAC
				AAGTGCCGNTAATTAAACTATAGGTAGTATATTAANCAAAAATGNGTTTTTNGCAATTATGIGAAAT
WI-6955b	79 GA	V	:	AAGGCTITAACCAAAGC
				TTTTTATGAAACATTTCAGATTCCCTCATATCACAGCACTCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC(G/A)NGTCATGTCCCAAATTCCCAATCCTAGGTAAGATATCAAAGTAACAAATTAACAAATTAAACAAATTAAAATTAAAATTAAAAATTAAAAATTAAAAAA
WI.6055	7.0	: 4		AAGTGCCGNTAATTAAACTATAGGTAGTATTAANCAAAAATGNGTTTTTTTTTT
200	?!			AAACTAAAAACCCTTATTGTCTCCCAAGTGTGTGGGCAAAATAGAAATICGGTTTCAAATACTGAAATAATCACAAAA
				AAATCGGGTGGATAACGGAGTATAGTTATATGGCTTGAAGAACTGGATTGAAAACCACTTTAGG
WI-6957	47 C G	 		CTAAAATAAATGTATGAATAATGCATAGACTGTGTATCTAGAAAATCATGC
				ACTICTAGIGCCTCTGTTACCACCACTCTAATGCCTCTGGTCGCCGCACTTCTGATGTCCGTAGGCCT
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	- c			CTCTCCTGATGGTGGGCCTCTGTTGJGCTCTTCTGTTCCGGTCGGATC
9669-IM		!		TRAGAGAGAGAGAGAGATGCTGCAGTTCCAAAAGAAAGGTTTCTTCCAGAGTCATCTACCTGAGTC
				CTGAAGCTCCCTGTCCTGAAAGCCACAGACAATATGGTCCCAAATTGAGCCGGACTGCACCTTCTGTG
_				CTTCAGCTCTTCTTGACATCAAGGCTCTTCCGTTCCACATCCACAGCCAATCCAATTAATCAAACC
W. 7021h 112 GA	12 GA	<u>·</u>	;	ACTGITATTAACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGIIA
2011				TGGGGAGGACAGGGAGATGCTGCAGTTCCAAAAGAGAAGGTTTCTTCCAGAGTCATCTACTGTG
				CTGAAGCTCCCTGTCCTGAAAGCCACAGACAATATGGTCCCCAAGIGCCCGAAGTGCAATTAAATAAAACC
				CITCAGCICITCITGACATCAAGGCTCTTCCGTTCCACATCCACACCCAAICAAIIAAICAAACC
	- 0		;	ACTGTTATTAACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGG11A
WI-/021	5	<u>.</u>		GCCAGTAGGACCACCAGTGTGGGGTTCTGCTGGGACCTTGGAGGCCTGCATCCCAGGATGCGGGTGG
		_		CCTGCAGCTCCTCCACCTCACCTCCATGACATGCTTGGTGACTTGGTGACTTGGTGAGCTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT
				GGGGCTGTTGAAGTCACCTTGTGTGTTCCAAGTTTCCAAACAACAAGAAGGTCATTCCTTGTGTGTTTCCAAACAACAACAAGAAAGTCATTCCTTGTGTGTTCCAAACAACAACAACAAGAAAGTCATTCCTTGTGTGTTTCCAAACAACAACAACAAGAAAGTCATTCCTTGTGTTTCCAAACAACAACAACAAGAAAGTCATTCCTTGTGTTTCCAAACAACAACAACAAACA
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				GTCCATGGAGAAGGCATATGGAGAACATGTTTTATACTGCTCTATAAATAGTATTCCAATCACTGTGT
	. –			CTTAATTTAAATAGCATT[ACJTCTTATCATTATCAGCCTTTTATGTATTTTCAAGIAAAAIAIIA
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				GGGACGCCTGTTGTTTGGCTCAATTTGGGTTTGTTGGTCACATGGAGCTCTTCCATTGCATTGACCGTGCCCTGCCGCAAAGCCCATGCCCTGCCG
				TGGTGGCAGCTGGGGCTGTGGATGGGAGGGGGTCCCCAACATGGATGTGTTGCCCCTCCTCCGGATGC
WI-7146c	210 A G	- 1		ACGCIAGIGTTCATGTACAAGGCCCCTCTGCAACTGGAGAAATTA
	: : :			GGGACGCCTGTTTTGGCTCAATTTGGGTTGTTGTTGTCACATGGACCCCAAGCCCATGCCCG
				AATAATGAGTTGTTCCTAGAGGAGAGAGAGAGGTCOCOAACATGGATGTGTTGCCCTCCTCCGCATGCC
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				TATAAAATGGCAACTGATAGTCAATTTTGATTTTTATTCAGGAACTATCTGAAATCIGCICAGAAGCCI
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				GCCTGCATGCCATTAACACCCAGCTGGCCCTACCCCTATAATGATCTGTGTCCTGTGTCCTAAATTATATTCTAG
				CAGTGGTTCCTCCTCCTGT/IGITAAAGACTAATGCTCAGAIGCIGIIIACGGAIAIIIACIGGAIGCIGIIIACGGAIAIIIACGGAIGCIGAIGAACTGCTCCCTGTAGAIACAAAAAAAAAA
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1001 /-IM	DEGI /-IM			CTCCTAGACTAGTGCTTTACCTTTATTAATGAACTGTGACAGGAAGCCCCAAGGCAGTGTTCCACACACTGTGAAATAAACAATAAAAAAAA
		-		ATAACTTCAGAGAAGTCAGTTGGAGAAAATGAAGAAAAAGGCTGGCT
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				TGTATCAGGTCAGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCCTCTGAGCCCAGCTGCCTGGAG
				AGGGTCTCGCTGTCACTGGCTGGCTGCTAGGGGAACAGACACACAG I GACCACAGAAAAAAAAAAA
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				TACTTGAGGCTGCCAATTACCAGCCCACGTTTCAGCTCAAGAGATGCCTTAAGATAATTATGTGAGG
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				GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCACCAAAAGCTTGATATACAGAAAAGAAAAGAAAAAAAA
				AAGGCTCAAGAATTTATTCACCAGTTCCTCTGCAACCCA(CA)TCTGAGCCIAICICICCICCIATI
				TACTTGAGGCTGCCAATTACCAGCCCCACGTTTCAGCTCAAGAGATGCCTTAAGALAALLALGAGG
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				ATAATTGCTTGTTTTCTAGCCTGGCAAGATATTTTCATAAAAGAGGGATAACAATGCTGATTACTAC
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				OCCAGTGGTGAACAGAACCTCCCAAATTTGAGTTGCACCCTTCCCTGTGGCCTTATGAGCTCAGCCTC
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WI-7743d 275 CT	75 CT	;		TTAAATGAGTGTTTTGTCACCGTTGGGGATTGGGGAAGACTGTGGCTGCTGGCACTTGGAGAGCAAGT
				GTTCAGAGACTCAGGGCCCCAGCACTAAAGUAGTGGACACTCAGAAGACTCATCCGAGGCAGGGTCAGGA
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				GTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACJCAJCCAGGAGTCCCTGGIAAIAAUIAUI
				GTGTACAGAATTCTGCTACCTCACTGGGGTCCTGGGGCCICAGAGCCICAGAGCCTCTCAGGC
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				GTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAACUCUAAGAAGTCACAGAGCAGAG
				TACAGAATTCTGCTACCTCACTGGGGGGCCCCCCCCCCC
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			TTAATTTACTGATTCCAGCAAGACCAAATCATTGTATCAGATTATTTTAAGTTTTATCCGTAGTTTT
			GATAAAAGATTTICCIATICCTTGGTTCTGTCAGAGAACCTAATAAGTGCTACIIIGCCAIIAAGACA
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			CAGATOCCAGCTTCGGCATTTGATCAGACCAAACAGTGCTGTTTCCCGGGGAGGAACACTTTTTAA
			TTACCCTTTTGCAGGCACCACCTTTAATCTGTTT[I/C]ATACCTTGCTTATTAAATGAGCGACTTAAA
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		-	ACATTGGTCATTGTGAATANNNNNNNNNNNNGCCAAGGCTAATCCAATTATTATTATCACATTTACCA
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			TGACGGTGGAATTTAA(G/A)TTTAGGGTCCCTAAAAGCATTTGACACAGTTGTTGATTGA
			CCAAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTTCAGGCCCGCTGCUGULTAGAATATGTGAATGTGAATGTGAATGTGAATGTGAATGTGAATGTGAATGTGAAGTGAAGCTCCCTTCAGGCCCCGCTGCCTGC
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				TGTCTTGTGTTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC
				ATTGCTTACAAGCCTAAGAATCTTTAGAGAAGTATACATAAGTTTAGAATAAGAATAAGAATAAGAATAAGAATAAGAATAAGAATAAGAATAAGAATAAGAATAAGAATAAGAAATAAGAAATAAGAAATAAGAAATAAGAAATAAGAAATAAGAAATAAGAAATAAGAAATAAGAAATAAGAAATAAGAAATAAGAAATAAGAAATAAGAAATAAGAAATAAGAAATAAGAAATAAGAAATAAGAAATAAGAAATAAGAAATAAGAAATAAGAAATAAGAAATAAGAAATAAAGAAATAAGAAATAAGAAATAAAGAAAAAA
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				GCTATCACAGGGTCACCTCTTTTACAGTTAGAAACACCAGGCCAGAGGCCACAGAATCCCATTCC
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			ACGICTTAGAACCTTCACCACAAGGAGTTTTTCTTGTAGTGATTCTCAAAGTCTTGGTAGGCATTCGA
			ACTGGTCCTTTCACTTTGAGATTCTTTTGCGCCTCTTATCAAGTCAGCACACACCTTTTCCAAG
WI-8021b 57 CT-			GATTITACGTTGCGGCTTGTTAGGGGTGATTCGGTGAATTGCCA
			ACAATCTCAGAAGGACTGTGCAAGTCAATGAGTCGCTTGTGAATTCTCATCTGGAAA(C/T)GATCCC
			ACGICTTAGAACCTTCACCACAAGGAGTTTTCTTGTAGTGATTCTCAAAGTCTTGGTAGGCATTCGA
	•		ACTEGICCITICACITICAGATICITITICITITIGCGCCTCTTATCAAGICAGCACACACCTTTCCAAG
WI-8021 57 CT -			GATTITACGTIGCGGCTIGTTAGGGGTGATTCGAATTCGGTGAATTGCCA
			CTGAAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTTCCACAGACACAGTCAATGTCAGTCA
			GCTTGTATTCAGGAGACAGGGCAGAGGGATCCCAGTGGCACTTCCCATGGGAAGACAGAAGAGAGAG
			GGGCCCCAGAGATGGAAGGACCCCAGTGTCATCACCAAACAACCATTTCAGCCGCTCTAGCCTCTAA
WI-8024C 206 A G -		:	TTCCCIAGICTCTAGAACAGCTGGCCCTGGTCGTCAGTACACAAGGAAAGAGCC
			CTGAAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTTCCACAGACACAGTCAATGTCAGTCA
			GCTTGTATTCAGGAGGACAGGGCAGAGGGATCCCAGTGGCACTTCCCATGGGAAGACAGAAGAGAGT
			GGGCCCCAGAGATGGAAGGACCCCAGTGTCATCACCAAACAACATTTCAGCCGCTCTAGCCTCTAA
WI-8024b 206 A G	:	;	TTCCC/A/GICTCTAGAACAGCTGGCCCTGGTCGTCAGTACACAAGGAAAGAGGC
			GAATGAGOCTTCCTAGCGCCGAGGGACCTGCTGCTGTTGTTGGCCTGCACATGCATTCTATGGAATGC
			TTTTTGGCCAAGCGGGGGCACTGAGGACTAAGCTCTGANNNNNNNNNN
			AAGGAGTCTGGGGTGTCATGCCCTACAAACCJAGJTAAATTCTCATCAGATGGATTTTATTTAACGTT
WI-8077 167 A G			GTGTATTGTGACTTACTTTCCAATCTGACTCTGGCATAACAAGGGAAAAA
			TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGAATGACCACTCCCTTGCTAAGGAAGCTAT
	•		GTACTTCATGCTGTGGAAACTGGCAAATACAGAATGTAGCTTGTTTJG/CJTTTTCTTAGCCTTGAAGA
			TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCCTATTCCTTCTT
WI-8118f 114 GC	:		AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
			TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGAJAGJTGACCACTCCCTTGCTAAGGAAGC
•			TATGTACTTCATGCTGTGGAAACTGGCAAATACAGAATGTAGCTTGTTTGT
			TGACCAGGTAGAGAGAGAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCCTATTCCTTCC
WI-8118e 40 A G	:		AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
			TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGAATGACCACTCCCTTGCTAAGGAAGCTAT
			GTACTTCATGCTGTGGAAACTGGCAAATACAGAATGTAGCTTGTTTGT
			TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTTCTGATTTCCCTGCTCCTCCTATTCCTTCC
WI-8118d 118 T.G	:	:	AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA

				·	TCTAGGITTAATCAAAGCAATTIGCANTTIGGATTTIGGAATGA(C/I)CACTCCCTTGCTAAGGAAGG TATGTACTTCATGCTGTGGAAACTGGCAAATACAGAATGTAGCTTGTTTGT
WI-8118c	44	- 1-0			IGACCAGG AGAGAGACAGGIGAGACCACAGTI ICCAGA I COMO AAAAATCAGACTCAAAGACTCAATGA
					TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGAATGACCACTCCCTTGCTAAGGAAGCTAT
_					GTACTTCATGCTGTGGAAACTI/CJGGCAAATACAGAATGTAGCTTGTTTGTTTGTTAGCCTTGAAGA
					TGACCAGGTAGAGAGAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCCTATTCCTTCTTCTTCCTTC
WI-8118b	88	0		1	AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
					TTTCTCTCCTTCCGGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGCAGGGGCCTCGGGAAG
					AGGGGTAGGAGGACOGAGCAGCATTCTCTGTAGAGGAAGACAGGAAAGGAGACCCTCTTGGCACACACA
	-				TTTATGGAGGGTTGTCCCTGAAGAGAAGGGCAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAGGC
WI-81714 299 CT	299				ACCAGTGGGCAAAGAGCACAATGAAGAGGATGATGATAAAAACAATCACGGCA
					TTTCTCTCTCCTTCCGGGGGACCAAGGTACCTTCTGGGGCATACAAC(A/G)TGGCAGCAGCAGCGGGCCTCGGG
					AAGAGGGGTAGGAGGACCGAGCAGCATTCTCTGTAGAGGAAGACAGGAAAGGAGACCCTCTTGGCAC
					ACATTTATGGAGGGTTGTCCCTGAAGAGAAGAGGCCAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAA
WI-8171c	46/				GGCACCAGTGGGCAAAAGAGCACAATGAAGAGGATGATGATAAAAACAATCAC
	-	-			TITICTCTCCTTCCGGGGGACCAAGGTACCTTCTGGGGCATACAACAAGAGTGGCAGCAGGGCCTCGGG
					AAGAGGGGTAGGAGGAGCCGAGCAGCATTCTCTGTAGAGGAAGACAGGAAAAGGAGACCCTCTTGGCAC
					ACATTTATGGAGGGTTGTCCCTGAAGAGGAGGCCAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAA
WI-R171a	46 A G	<u>8</u>	,		GGCACCAGTGGGCAAAAGAAGCACAATGAAGAGGATGATGATAAAAACAATCAC
					TITICTCTCCCGGGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGCAGGGGCTCGGGAAG
		_			AGGGGTAGGAGGACCGAGCATCTCTGTAGAGGAAGACAGGAAAGGAGACCCTCTTGGCACACA
				_	TTTATGGAGGGTTGTCCCTGAAGAGAAGGGCAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC
WI-8171b 298 T	298	 	•	;	ACCAGTGGGCAAAGAGCACAATGAAGAGGATGATGATAAAAACAATCACGGCA
		<u>:</u>		: :	GAGGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTGCAATTGAGCACATTTCTTGGGTCTGT
		-			TTCTCTATCTCTAAGGG G/CJAGTCTCAAAACCCCCAGCTCAAAATACGACACTAACATGATGAACAT
		_			GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAAGAGCACTGTCCAATAGAACTTTC
WI-8314b	85	S			TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAACCACT
		<u> </u>			GAGGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTGCAATTGAGCACATTTCTTGGGTCTGT
					TTCTCTATCTIC/GJTAAGGGGAGTCTCAAAACCCCAGCTCAAAATACGACACTAACATGATGAACAT
					GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAAGAGCACTGTCCAATAGAACTTTC
WI-8314	78	78 CG	1	:	TGTGATGAAAAAAATTCTACTTCTGACCTATTCAATAGGGGTAACCACT

	-			TTTTTAAATATGCCCGTTTAGAGCAGACACAGTCACAATAAAAGTTAAAAAGTTACAATGTCCAG
				TGTATATACCCAGGNAATCCATTCTTGGTACTTTTCAAGAGCTGCTGTTATACTGAGAGTCTCTGAGAAG
WI.8321	1786		i	TCCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTCAGAAT[GAJAGIAICIIAGIAIUIIUA TTTTGCTATGGTTCTAGTTTATCAACCTACTTTATTAGCTGAACTGTTGGC
1) ;			TTTTTAAATATGCCCGTTTAGAGCAGACACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG
1000	178			TCCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTCAGAAT[GA]AGTATCTTAGTATTCTTGTATTCTTTGTATTGCTAGTTTATCAGCTACTTATTAGCTGAACTGTTGGC
7	2:		!	TATGTACTCACTTTCAGTTACCCCCGTGCCTCCAGAATCGCATGTTGCTCCACCTGGGGGGGG
				AATTACCTCTAGATTGTCCAAAGCCCAGTCTTTCCCTTCCCTGTGCAGCCTTAGAAVCACTAAGTAG
WI-8332b	123	: O	:	AGGTGGAGGGINTCCGGGGAAGCAGTTAGATTAAGTGTGATGCACA
	il.	, -		TATGTACTCACTTTCAGTTACCCCCGTGCCTCCAGAATCGCATGTTGCTCCACCTGGGGGGGG
				AATTACCTCTAGATTGTCCAAAGCCCAGTCTTTCCCTTCCCTGTGCJACJGCCTTAGAAACTAAGTAG
				CAGTACTGTTTGGTGTTTGTTTCTTCCCCAGCAATGCCTACTGCAGCTACTTAGTAACAACTAG
WI-8332	114	AIC		AGGTGGAGGGTNTCCGGGGAAGCAGTTAGATTAAGTGTGATGCACA
!-				TGCGGGCTTAACAGGAAGCATGACTGGGAGGCCTCAGGAAGCTTATAATCATGGCAGAAGGCGAAGG
				GGAAGCAAGGACCTTCTTCACATGGCAGCAGGAGAAGAGAAGAAGAAGAAGGAAAGTCTACACATTTT
				AAACAACCAGATCTCATGAGANTTCCATCGGGAGACAGCACTAGGGGGATGGCACTAAACCATTAGA
WI-8378b	311T	0	:	AACTGCCCCATGATCCAATCACCTNTCACCAGGCCCCTCCTCCAACACGIGGGG
				TGCGGGCTTAACAGGAAGCATGACTGGGAGGCCTCAGGAAGCTTATAATCATGGCAGAAGGCGAAGG
				GGAAGCAAGGACCTTCTTCACATGGCAGCAGGAGAAGAGAAGAAGGGAGAAGTCTACACATTT
				AAACAACCAGATCTCATGAGANTTCCATCGGGAGACAGCACTAGGGGGATGGCACTAAACCATTAGA
WI-8378	308	T C	1	AACTGCCCCCATGATCCAATCACCTNTCACCAGGCCCCTCCTCCAACACGTGGGGG
				TTTAGCACATATTTAGCATTAAGCCTCAAACGATACAGCAATATGTTACATTCTCTTGTGAAAACAG
	_			TTGTTGTAGACTGTTAANNNNNNNAAATGTAACTCCGACTTGTGCCTAATAGGATTTGACCNTTAA
				GAGGNITCTTTTGCTGTGGANGGGGTGGCTTTGCTTGAACTTCCATTCTGT/GJGCCTTGTAGCTGGTG
WI-8426	184	1 €	•	AGGCTGGGAGTATGGANGGNCCCGGGGCCCTTGGCNATNGNATTCAGTGAG
	:			TTGAGCCTCCACAAATAATGCAACCAAGTTTTACATTTTTAACAGCCCTTCTACATACA
				TCTTCTCTATCTTAGTTCCAAGTTTTAGTTTTCAATCCCAATTATACCAATTCCATTGTTATTTAAGA
				AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCTCCACTACCCAGCAAACIAC
WI-8450h		61 C.A	;	AGAGAGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATICAT

				TTGAGCCTCCACAAATAATGCAACCAAGTTTTACATTTTTAACAGCCCTTCTACATICJACACTCCAT CTTCTCTATCTTAGTTCCAAGTTTTAGTTTCAATCCCAATTATACCAATTGCTATTGTTATTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAGCTAC
WI-8450g	55 T C			AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAT
				TTGAGCCTCCACAAATAATGCAACCAAGTTTTACATTTTTAACAGCCCTTCTACATACA
				CICTATCTTAGTTCCAAGTTTTAGTTTTCAATCCCAATTAGTAACCAATTCCATTGTTATTAGCTTACCAATTGTTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACCAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAATTACAA
WI-84501	108 T A	:	ţ	AAAAACCITCCCAGIIAIIGICAGAAACATAIGAIIIAGCITAATGCCAATTCAT AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAT
1				TTGAGCCTCCACAAATAATGCAACCAAGTTTTACATTTTTAACAGCCCTTCTACATACA
				CTCTATCTTAGTTCCAAGTTTTAGTTTTCAATCCCAATTATACCAATTCCCATTGTTAfT/C)TTTAAGA
				AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTAACCCTCCACTACCAAGAAACTAC
WI-8450e 125 T C	125 T C			AGAGAGA I GGGAGI GI ANINI GAGGAGI ACAGAGA GAGAGA GA
				TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTACAAGCCCTTCTACATGTTGTTTAAGA
				AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCAGCAAACTAC
WI-8450d 125 T C	125 T C	:		AGAGAGGATGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAT
				TTGAGCCTCCACAAATAATGCAACCAAGTTTTACATTTTAACAGCCCTTCTACATACA
				CTCTATCTTAGTTCCAAGTTTTAGTTTTCAATCCCAATTAT/AJACCAATTCCATTGTTATTTTAGATCCAATTGTTAGATCCAATTGTTAGATCTAGATTAGATTAGATTAGATCAATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAG
				AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTAACCUUUUUUUUUU
WI-8450c	108 T A		:	AGAGAGGAI GGGAGIGI MAI AI GAGGAGIGI MAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
				TTGAGCCTCCACAATAATGCAACCAAGIIIIACAIIIIIAAAAGGCCTCCAATAACAATAACAATAACAATTATAACAATTGCATTGTTATATAAGA
				AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCCTCCACTACCCAGCAAACTAC
WI-8450b	61		<u>:</u>	AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAT
	1			TTGAGCCTCCACAAATAATGCAACCAAGTTTTACATTTTAACAGCCCTTCTACATTCACACTCCAT
				CTTCTCTATCTTAGTTCCAAGTTTTAGTTTTCAATCCCAATTATACCAATTCCATTGTTATTTAAGA
				AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC
WI-8450a	55TC			AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAT
				CAAGGAAAGCTGTCAGTCTTCATAAACTTTCAAAGAGTTACAAAAATACGTATTTTTAA(A/G/G/TA
				CAATTCAAGATTAGCATOCAAACCTACAAACATGATGTACATTCGTCACACACACACA
				ACCTGGCTACAGCAATGTTGACTTACATCACCATTGT11A1AC11G1GAAAAC111A11G1GCACAG
WI-8458b	60 AIG			GACATCCATTCCGCCAGACTAATGTTATAAAGCAGCTGAAGCAGAAAGTTCTCA

			CTTCCTCCAAAATCTACATGAATACTTGAAGACAATATAACTACAACCTTACAAATGCCAATTA GACAAAGAGAATAAATGATATAAATATAAATCATTTTT[AT]NNNNNNNNCCTTGTCTTATTCACAT
Wi-8461c	105 A T		TCAGGGAAGTCTAGCACCAAGGACAGTNITAACAACATTACAANTTINTAGAAAAGTTATTACTTA AAACATCTGTGTGACGTACATCAAAGAAAAAAAATCAAGGATTTGCAAAAAGGAAAGAAA
			CTTCCTCCTCCAAAATCTACATGAATACTTGAAGACAATTCJATAACTACAACCTTACAAATGCAAATTAAATATAAATATAAATTATAAATTATAAATTATAAATTATA
WI-8461b	38 T C		TCAGGGAAGTCTAGCACCCAAGGACAGTNTAACAACATTACAANTTNTTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAAAAANTCAAGGATTTGCAAAAAGGGGG
			CTTCCTCCTCCTCAAAATGATACTTGAAGACAA(T/CJATAACTACAACCTTACAAATGCCAA TTAGACAAAGAGANTAAATGATATATAAATAAATTAAATT
WI-8461	38 T C		TCAGGGAAGTCTAGCACCCAAGGACAGTNITAACAACATTACAANTTINITAGAAAAGTTATTACTTAAAAANTCAAGGATTTGCAAAAAGGGGGG
		! !	CTTCCTCCTCCAAAATCTACATGAAATACTTGAAGACAATATAACTACAACACTTACAAATCATATAATAATAAT
WI-8461	105 A T	. !	TCAGGAAGTCTAGCACCAAGGACAGTNTTAACAACATTACAANTTNTTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAAGAAAANTCAAGGATTTGCAAAAAGGGGG
			AATAACATGTTATGAAACAAGCTGGTTACAAGTAGTAGGTAG
			TAAAAAGCAT[AG]AACATGCATATAAAAATTAGATTATGTACAAAATACCAACAGTATTTAGATATTCTGAAAAAAAA
WI-9438	77 A G		ATCAGAAAACATGATCGTGGAGAGAATTATTA
		-	ACAGAAATTGACCTTTATTTGTTGTACTAAAGCCTGTTTAACTTTTGATACAAGTAACATTTAGTA CAGAAAATCCCAGTCTGTCAGTCAGTACCTGT[C/1]TGTGCACTGTACCAGTTCCAGTCCCACTCT
WI-9439b	101 C T		GCCTGTAGAAAACAGCCCCTACCCCAGAGGGTCTGCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTTCATAGTTTGTCTGAGCTAGAAAACTTGTACCTGTAAAACAAAG
			ACAGAAATTGACCTTTATTTGTTGTACTAAAGCCTGTTTAACTTTTGATACAAAGTAACATTTTAGTA
			CAGAAAATIC/TICCAGTCTGTGAGCTCAGTACCTGTCTGTGCACCTGTACCATCTCAGTCCCACTCT
WI-9439a	76 CT		CAGITITICATAGITIGICTGAGCTAGAAAACITGTACCTGTAAAACAAAG
			GAAGGCTTGATTAAGGGAGGNTTTATTTGATGTNAACTTACCATTCCATAGACTATAAAGANCATTA
			TAAAAAATICJCCTCTAAAGNGACACATGCCCCCAAATGACCANGNCATAAGCAAACCTTTTAAAT
	1		TACTCATCTTTCATATGTGTGTTTGTNCCCCTACTNTTATCACTGTGTCTTCTGTCTTTGTCTACCTATATGTCT
WI-9446b	WI-9446b 75 TIC	:	IGNEANCIGCACACIAICIGIGGCAAIAIIGI

-	-			ATTACACTACACTACOCATACOCATACACTACACTACAC
				GAAGGCTTGATTAAGGGAGGNIIIAIIIGAIGINAACIIACAIICCAIAAACAAAAAAAAAA
				TAAAAAA[T/C]CCTCTAAAGNGACACATGCCCCAAATGACCANGNCA AAGCAAACCTTTAACTA
		-		TACTCATCTTTCATATGTGTTTTGTNCCCCTACTNTTATCACTGTGTC11C1G1C1111G1C1ACCIA
WI-9446	75 T C		:	TGNGAACTGCACATATCTGTGGCAATATTGT
				ATTAAAATGICAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAATGGTATATATA
				GAGATAATTATTCTAGATTCCAGGCTTTCTTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA
				TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCTTTAATTAATCAAAGTATGTTAATGICAC!!
WI-9497b 185	85 A			GGAATTCTACATGGAAAAAGCCAACAAAATAACTAAAACTTGACTAATGAAG
	Ε.			ATTAAAATGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAATGGTATATATA
_		•		GAGATAATTATTCTAGATTCCAGGCTTTCTTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA
				TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCTTTAATTAATCAAAGTATGTTAATGTCACTT
WI-9497	185 A		:	GGAATTCTACATGGAAAAAGCCAACAAAATAACTAAACTTGACTAATGAAG
_			:	GTGAAAAAGTTTTCTATTCATTCCATCATACAATAGATTGTGCTAAGGATCATTTTGGAAGAATGTG
				CAGCATTCAGAAGTTGTATCTCATCATGCAGTCACTCAGCAGCATTTTATCTAAAAGTACGTGCACA
				GACTCAGACAATTACAAACTATTTCAGCCATGATCTATGGTGATTTTCCACACATTGTA[C/A]AGTG
140000	V C C C		-	AAAGCTCTTCAGCTTGGAACAACTTGTCAAGGCAGACTGCATGCA
WI-95.55	5			GTGAAAAAGTTTTCTATTCATTCCATCCATACAATAGATTGTGCTAAG(GAJATCATTTTGGAAGAAT
				GTGCAGCATTCAGAAGTTGTATCTCATGCAGTCACTCAGCAGCATTTTATCTAAAAGTACGTGCA
				CAGACTCAGACAATTACAAACTATTTCAGCCATGATCTATGGTGATTTTCCACACTTGTACAGTGA
	7		;	AAGCTCTTCAGCTTGGAACAACTTGTCAAGGCAGACTGCATGCA
WI-95238				AAAAACAAGAAGTTTCATACATCACAAAAAACCTTCCATTATAACACAGAAGTGATTATTACCAGAC
				AAGCATCAGTGATGTATGTATGCTGCCTTTNCTAGTTGTTATTGTACAATGCTGTAGATAATGCAGCCCATG
				CAATACACCCAAGAACACTAGAGTCCTACACCCAAGTACAATATGATAAAGCAGCCCTCTGCAAGTG
	1			GTICIGCTGGATACCACTAAGAAGTCTACTGCAGCCATGTTGGTTATGATTTT
+CCR-IM	2			CCAAAAGCCAAACCATTCATATGTATGGATTTCATAAACATTTATTGATCCTTTTTTGAGGTAAGTAT
				A A A TACCTITACATEGECT A A CETT CTA A CIGA I CITE A A A A A TACCATITICA A G G A CTETT A A TE A A A TACCTITICA A G G A CTETT A A TE A A A TACCTITICA A G G A CTETT A A TE A A A TACCTITICA A G G A CTETT A A TE A A A TACCTITICA A G G A CTETT A A TE A A A TACCTITICA A G G A CTETT A A TE A A A TACCTITICA A G G A CTETT A A TACCTITICA A G G A CTETT A A A TACCTITICA A G G A CTETT A A A TACCTITICA A CTETT A A A A TACCTITICA A A A A A A A A A A A A A A A A A A
				GTTAAATAATCTGCTTTAGAAGGCACAAATGATCATACTTCAGATTAAAATACAGGTAAGTATTCAG
1811 05.55	0.7		<u>;</u>	GGNTAAAATGGTACAAAAAGGCTGTAACTCTTTTNCTTCACATTGATCACA
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				TABACAATAGCTACCATATATTTGTATCTNCTCCTTGGGAAAAAACTTTGGAAAAAAAAAA
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WI-9625	172 A T		_;	AGTAGCACAGACTAGTTATTCATTTAAAAAACACACTGACAAATCTTTC
:				TTTTCTGAGATICAAAGAGCTACATTTTTGGTTAGTGTATGTCTACTATACCTTTTTCATCCTTTCA
				ACATCTTTTGTCACATTTTAGGTGATGCTCTTGTAAACAGTGTATTGCTAGACCTAAAAATCCAAGCT
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WI-9647	144 CT	:		ACTIVATACGICICITICAGAIGICCCIGCTITITAGITAATIGIGITI
				GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAAAATTGGCAATCTTTTA
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				COCATTTCACCTCAAGGCATCTTCAGCAACCCCACATGGCTTCCCTCTGTGCGCATGAATAACTTGA
WI-9676n 114 A G	114 A G			GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTT
				GECCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAAAATTGGCAATCTTTTA
				GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGGAAGATGTGGCTTTCCTGCCCCC
				ATTTCACCTCAAGGCATCTTCAGCAACCCCACATGGCTTCCCTCTGTGC(G/TJCATGAAATAACTTGA
WI-9676m 184	184 GT			GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGT
				GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAAAATTGGCAATCTTTTA
				GGGGTACCAAGGINTCTG/AICIGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTGC
				CCCATTICACCTCAAGGCATCTTCAGCAACCCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA
WI-9676I	84 A C		:	GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTT
				GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAAAATTGGCAATCTTTTA
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				CCCATTTCACCTCAAGGCATCTTCAGCAACCCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA
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				GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCCC
				ATTTCACCTCAAGGCATCTTCAGCAACCCCACATGGCTTI/CJCCCTCTGTGCGCATGAAATAACTTGA
WI-9676i	173 T C			GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGT

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			GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAAAATTGGCAATCTTTTA
			GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGGCTTTCCTGCCCC
			ATTICACCICAAGGCATCTICAGCAACCCCACAIGGCTICCCICIGIGCGCAIGAAAIAACIIGAGG
WI-96760 202 CT	:	:	C/ICAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGT
			GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAAAAATTGGCAATCTTTTA
		•	GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCCC
			ATTTCACCTCAAGGCATCTTCAGCAACCCCACATGGCTTCCCTCTGTGCJGAJCATGAAATAACTTGA
WI-96761 184 GT	:	:	GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTTTGT
			GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAATTGGCAATCTTTTA
			GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCCC
			ATTICACCTCAAGGCATCTTCAGCAACCCCACATGGCTT7CJCCCTCTGTGCGCATGAAATAACTTGA
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			CCCATTICACCICAAGGCATCTICAGCAACCCCACATGGCTTCCCICTGTGCGCATGAAATAACIIGA
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				TGGACCAAACACAGACAGATGTATTCCTGGTGCCTGTGTAJCAJATTACAACTCATTGATCACTGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAAACACAGTAAATGACTCCACATTTTCCCTTT
WI-9738b	40 C	;		GAGTCAACAAAAGACTCTGCTTGTCACCTTGCCTGGAGCGGGGTGGTTTTCACTATGTGAGTATCTA TCTTTTATTTCTGTCCCTTATGTTGGTGGGCACATGTCTGTATTGCTGTCC
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				ATAATTGACTTTGCTACTGGAAGAAGTCTTAGAATGTTGGAATTTCTCTATTACACACTTTGCCTCA
WI-9778	127 GA	:	:	AAGAATGTGTCAGTCAGGACTAAAGGCAATAGTCTCAGGGCAGACAGCC
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				CCATCTGCATCAAAATCACCTGCAGGACTTGCTGACAATGCAGTTTCJCAJTGGATCCCACCCAGGA
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157 CA			_		GAACTAACACCTTTCTTGCATGGATTTTTCTTGATTATTGGCAGTTAACAATAAAATGTTATTAGATCACTAAACACATAAGGGAGGCTGTGAAAAAAAA
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=	115 CT		AGCTTGACCTAAAAGGGACCTGTGTGAGCATTTCAGATTGAGC
ESTC1	33	:	CCCTGTA <u>GCAGTCTTCAGCCTCCTTACCCTACNAGATCTGGAGCAACAGCTAGGAAA</u>
ESTC102	37		GCTACTACCACGGCTGCTTCGTTTGGACAAAATAACNAGGAGGCATCCACGGGATTAGTTA
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			AAGGGACACAGTGTTGCTGACAAGGTGACACTGAACANAACAGTTTTCCTTTAATTGTAAAAGCGGG
ESTC113	37		CATCG
			AATTGGCTCTTCTCCACATGATACNTAAGTTCAAGGTCCAAAGTTCCTATCACAATTTACAAAAAGG
ESTC117	24	:	CTCCA
ESTC119	24		TGTCAAGCAGATCTTGAGGGTTAINGTTAAGCCTGATAACAGCCTCTTT
			GACAATAAACAGCTAAGCTACTGACATAAAATATNCAATAAATTTATGAGATATAAGGTACAGATG
ESTC122	34		AGAAAAAICIGAAA
ESTC123		<u>;</u>	GAAGCCAGTATGTTGTGGAAANATTCGAGAAACACACTGAAAAA
			GCAGAGGCATCAGATAAGGCCTCAGAAAGCCCAGGCCATCATNTTCCATGGGACCAGGCTGGCTCAA
ESTC128	42	:	TGTGGAACTGG
ECTC 199		1	AGTCACCATGCCCAGCCTAGNATGAGTTTAGTAAGATTTGGTTATGCTGGGGAG
			GTGTATCTGGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAGNAGCAGGTGCCGAGGGTCTGGA
FSTC13	4. P.	.!	ТСАВАААА
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ESTC132	30	· ·	GGTAAAGICTAAATTACTGCCTTAGCAAACNCTATGTTGTCAGGTTTTTCTGCTGCA
ESTC137	21:		CCAGTITIGACTICTGTCCTCANAGTCTCTCCCATGTGGCAAACA
			AGGAGCACAGGCCTAAGGACATGAAGGTCAGAGTTTCTCAGAGAGGNGGGGGCTGGGGTCCCTGAGCIAG
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			CCCATTGTGGTCACAGGAAGNAGAGGAGGCCACGTTCTTACTAGTTTCCCTTGCATGGTTTAGAAAGC
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ESTC142	72		AAAGANACCATTCCTAACAAACA
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ESTC144	26	:	AAATCCATATTTCTTGACATGAGGTNGCTTTTTAGCAGCATTTCGG
ESTC146		1	CATGTCCAGGATAAGGAGCANACACCAGGATTTATACACGGTGGCAGCG
			TCTTTGGTTGTCTACACACACACTTAAGTACTGTATCGCTGTNATGCAGCGCCTGTGGAGGCCCTTG
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131066	-		TGCACTGTTACTOCCCAGACNGAGAGCTTACATACCATATAGAAAGAGCALAAULUCLLICAGAAAGAGCALAAULUCLLICAGAAAGAGCATATAGAAAGAGCALAAULUCLLICAGAAAGAGAGCATATAGAAAGAGCATATAGAAAGAGCATATAGAAAGAGCATATAGAAAGAGCATATAGAAAGAGCATATAGAAAGAGCATATAGAAAGAGCATATAGAAAGAGCATATAGAAAGAGCATATAGAAAGAGCATATAGAAAGAGCATATAGAAAGAGCATATAGAAAGAGCATATAGAAAGAGCATATAGAAAGAGAGCATATAGAAAGAGAGCATATAGAAAGAGAGCATATAGAAAGAGAGCATATAGAAAGAGAGCATATAGAAAGAGAGCATATAGAAAGAGAGCATATAGAAAGAGAGCATATAGAAAGAGAGCATATAGAAAGAGAGCATATAGAAAGAGAGCATATAGAAAGAGAGAG
ECT7225	30		ATGTGTAGGATCG
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ESTC23	27		TCCTGAAAGGG
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	+	1	CASTAGAATAAATCAAC
ESTC231	24		CAAAAGGGTTAGTCATATTCCCCANCAACAGCAIGAIAAAAAAAAAAAA

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				GAAGAGCTGGGCACGCATCTGACNITICTTCTTCTTATTCTATAAAATAAAAATAAAAATAAAAATAAAAAA
ESTC28	23			39
				CAGACATGACCTACCGTCCCNGGCCCTCAATTCATTTTATTCTTGAGCCGCTTGGTCAGGTTGATTGA
ESTC3	- 50			ICICACACICA
				ACAGCCCCACAGAACTATTGTAAAACAATATTNTCAGTCGGTGATCATTGTAATATACAAAU
ESTC31	32			CAATTICCICAGA
ESTC33	25			AGCACTTOCAGCTCCTTGACGTTGTNGGACCAGGGAACTTCCGGGAA
ESTC39	26	;		AAGGAAAGGGAACCTGGGGTTTNGGTCACAGAACTCAGAGCCTGGGCATTA
FOTCA				CCACTGAATCACACAACATGGACNAATCTCAAATCATTATGCTGATGGAAAGAAACCATT
ESTC40	22			GGCATGCTAGACAGAGGCATTANTTTTGAAGATCTTTTAAAAATATTTTGACTTGTTCCCCCTTCAC
ESTC 45	37			TTGGAGGTTTGTGTGTGGGGTTTTGTTGTACNCTCTCATCACGAGGCTATATTAA
				CTGTCCGTGGTGAGCCCTGCCGCTGTCCCATGGGCCCAGGGGAGCCACTGGTGCGGANCCGGGCAGATG
ESTCSO	56		1	TTTACCCTGT
	 			GTGCCCTGAAGATTAGCAGCAGCAGCAGCAGCAGGTGGCAGGAAGNAGTGGAGGGAAAGGACACCA
ESTC56	45		1:	AGT
ESTC57	20			AAGTGGGCCCTCCCAGTCCCAICTCTGGGCACAGATCCCACCAGTCTGCTC
				GAAACACAAAAGTGTTGAGAAAAAAACTTCTCAAAATTNGTTCCAGACTTCAGGAAAATGATTTCC
ESTC59	38		:	ACATGGTAAGGCC
				TCTGCAGCACTTCACTACCAAATGAGCNTTAGCTACTTTTCAGAATTGAAGGAGAAAATGCATTATG
ESTOS	27			TGGACTGAACCG
				AGTGATTTTGGCTAGGCGTGGTTCTCATCTGTGAAATTCCACAGCGCAATGACAGCANCCICICICC
ESTC61	57		:	ACCCACTCAAG
				ACAGACACAGCATCACACCAVAGGGCCCACGGGAGGGTCGGGGAGACGACACTTTTTCCCTGGGAAA
ESTC63	20	;	:	GGCAGCTCTAATC
		:		GAGAGGCTAGTCAGGAGGGANACCCTCAAGTTTAAATCCCCACACTTACTTACTTACTGCTCATCCGT
ESTC69	20		;	CACTTICGCTAA
				AGTTTCCCTAGAGCTGTGCGGCCAGATAGCTGTTCCTGAGTTGCANGCACGATGGAGATTTGGACACT
ESTC7	45	!	:	0

ESTC72	37	_ ‡_	:	GGGCTTCCAAAATGGGGTTTTGGGGCCAGGAGGTTGGCHTTTGGCGTGACGCCTAAAAAGTGTGACC AACAATTCACAGGTACAGGAAATGTAGAACAAAATTCAATCATCACCTTGGGTTGAAAAGTTG
ESTC74	49	-	;	GAAGA
ESTC77	40			ATGACTTTCCTGTCCCATCGGAAACCAGAGTTTCCCCAGGNGAGCCCTTCCTATCTGCGGTTA
ESTC81	20			GGCTCAGCACAGGGATAAGANCCCCACTCCGCATGTCCCAGAGGGCAGCACTCCAG
ESTC®	25		•	GAGOCTGACOCA
E647003	6 4			CAAAATCAAATACACAGATCCAGATATGTGAACCATATATACATATCIAIACANCCAIIAIIIAAAC TTCACAAACCT
325	2			TTTAGCTGCTATACCAAGTTTCCATAAANCTGTCTGCTGGTTGGGGAGGCTACAGCCTGACCACATTC
ESTC85	28		**	тисс
ESTC89	22		: : :	ATTGCAAAGGAAGTGGAACGTGNTCAAACAGAAATGGTGACAATGA
ESTC90	33			CTGGTTCTCTTCGTCTTGGCATTCGTCCTCCTCNGGCCAGTGCTCCACCCCAAGTGTCCTTCCCGATGAT
ESTC93	5 8			CTCCCCTCCTCAGTTCACAGTGGAGGTANGGAGATTCAGGGCAGGATCC
ESTC95	32			GCACGПСТТGTTCTCCTCTTCCAGAAGTTGNAGACGTCTATTTAGTTTGATTATCTGTCG
				AAATGACTTGACGAAGCTCATAGAAGATTAGCAGGTAGTAGAATAATGACTGCTGACTGCTGATTCTCCTGACTGCAGGTGCACAGGGTCTCCCAGGTGCTCCCAGGTGCTCCCAGGTGCTCCCAGGATCCAGGAGGTCCAGGAGGTGCTCCAGGATGCTGCAGGAGGTGCAGGAGGATCAGAGATGCAGGAGGAGAAAAAAAA
DWII-100 127 GT	127	! 		ATTCTTATCAATGATCTTTCACCTAAGAAACAGCAAAGAI I U USUJAAGAAGAAGAAGATTATTGCGATTTTTCACAAAAATCAAAAGAAGAAAGA
				TTCCATCCTAGATATCTACTCAAAATAATTGAGACAAGTGTTCAAACAGAAAGACGCTTGTGCTGAA TGTTCATGGGJAGJGCCCTATTCACAGTAGCCAACGATGAAAACAACCCCAAGCTATATATCACA GATGAAAGGATAAACAAAATGTGGTCCATCCATACAATGGAGTATTACACAGCCATAAAAAGGAAT
DWII-177	77 A G			GAAGCAGTGATCCCTACTACACTGTGGAT
				CAAATACCTGGACTATCAACCTTGTTGCTTAATCCCTGCAGCTTCAAGGTTAATCCATCTAAG IGAC ATTTTTGAAATTCCAGCGGTGCCACCCAATCATGCCGCGCTTCTGTCATTGAATGAGGTACATTTTCATGTCTGGGACTTACAATATCTCAGGAACAGCAATG
DW11.286 213 AIC	213	<u>-</u>		A I BI CI GACCI CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRA
DVV C-FCC	3			

			AGTATACAAA	AGTATACAAACATITAAGCIGIGGICAAGGCTACAGATGIGCTGACAAGGCACTTCATGIAAAGIGT CAGAAGGAGCTACAAAACCTACCCTCAIAGIIGAGCATGGTACTTGGCCTTTGGAGGAACAATGGGC
	- (TGCATTGAAG	TGCATTGAAGATCCAGCTGCCTATTGATTTAAGCTTTCCTGTTGAATGACAAAGTATGTGGTTTTGTA
762-DMD	5 7			APPROXIMENTAL CONTINUE OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE
			GAACATICCI	GAACATTOCTOTGGGAGCACTTCACTACCAAATTAGCAACTACTTTCAGAAATTCTTTCT
			CAAGACAAAC	CAAGACAAAGCAAAGCCACATTTGCATTAGACAGATGACGGCTGCTCGAAGAACAATGTCAGAAA
DWU-330	85 CT		CTCGATGAAI	CTCGATGAATGTGTTGATTTGAGAAATTTTACTGACAGAAATGCAATCTCCCT
			GAAAATGTTA	GAAAATGTTAATTGGGCAGGTGAAAAGGGTACAGATGTGCTGTAGCAGACCTTTGGTTTTAAAAGAG
			AAGCATCATT	AAGCATCATTTCCCCAACAGGGCAACTGTAGAAGGCCCAGCTGAAGAGTAAAGGAAAAGGTCTGAGG
			ACTGAGCCTG	ACTGAGCCTGTGGCTGGAAAAAGGTGAATGTTGAGGGGCCCTTCACTTCCATCACAGAAAGTC
DWU-370 231 A G	231 A G	1	ATTAGACGG	ATTAGACGGTACCAATTCAGTGTCTGTTCCT[A/G]GCATCTATTTCCTCTGTGC
		_	CTCTTAACTT	CTCTTAACTTCAGTTCCCTCATCTATAAGAATAAGGGATTCAGTTGTGATCACATAGCTCAGGTAATC
DWC			CAGGACCAG	CAGGACCAGAAACCCAGGAGCJA/GJTGGGACCTGATCCACAGCTAGAGGATGGGGGACTCTGTAGCT
1537b	89 A G	<u>:</u>	ACAGCATTT	ACAGCATTTCCTGAACACACAAAATCCAGTAAGCAGCACACACTGGCTGA
	-		СТСТТААСТІ	CTCTTAACTTCAGTTCCCTCATCTATAAGAATAAGGGATTCAGTTGTGATCA(C/T)ATAGCTCAGGTA
DWC			ATCCAGGACC	ATCCAGGACCAGAAACCCAGGAGCATGGGACCTGATCCACAGCTAGAGGATGGGGGGACTCTGTAGCT
1537a	52 CT	:	ACAGCATTT	ACAGCATTTCCTGAACACACAAAATCCAGTAAGCAGACACACAC
			ACCATCTTAT	ACCATCTTATACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC
			CCCAGCTCC	OCCABCTOCACCCAGAGGCCCCTGGGGAATTCCAGGGTCACTGTTOCTTCCTGTCTCTGTGGGAAT
ESTO			CAAGCCAGC	CAAGCCAGCTCCAGGCCAGAAGTGGGACTGTGAGGACATGGAGGCCTCGGCACTGAGGTGCGGAGA
	196 C G	:	CCCGCAGAC	CCGCAGACCAACTCCTGAGCTTTCTGGGCCTCTGAGTCTTGTCCTC
			ACCATCTTAT	ACCATCTTATACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC
			CCCAGCTCC	OCCAGCTCCACCCAGAGGCCCCTGGGGAATTCCAGGGTCACTGTTCCTTCC
ESTD			CAAGCCAGC	CAAGCCAGCTCCAGGCCAGAAGTGGGACTGTGAGGACATGGAGGCCTQGAJGCACTGAGCTGCAGA
	184 GA	:	CCCCCAGAO	CCCGCAGACCCACACTTCTGGGCCTCTGAGTCTTGTCCTC
			тстсствтся	TCTCCTGTCATTCCTACTCCATTAGTTCAAGGTCAGTGAAGAACTGGGGCAATTAACCAAGTAATTCA
ESTO			TGGACTGCC	TGGACTGCCCAACTGCGAAACAAGAAGGGCGCAGTGGAGCAGGAGTATTATGCTACGCGGTACCTT
ANT	160 T C	:	TTTTATGGA	TTTTATGGAGGACCGAACTGAGGC[T/C]GAGCTCAGATGATCCTGT
			TGCCTGGG	TGCCTGGGGTGGCAAGGTGCAAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA
EST10398			AGATGCTGC	AGATGCTGCCACCTCTTATCTACTTGATGTTCACATTTGGGGGCTTGACTTTCCACACACGGAGAAG
2p	168 A'G	-:	САТТЕТТТ	CATTGTTTCTTCGGGCCAAGAAGGTATCTACCAAGAAGIGICIAIIAGGCAIIIG

				- * * C C * * C C C C C C C C C C C C C
				TGCCTGGGGTGGCAAGGCTGCAAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA
EST10398	_			AGATGCTGCCACCTCTTATCTACTTGATGTTCACATTTGGGGCTTGACTTTCCAACACACAC
2a	147 CT	:		CATTGTTTCTTCTTGGGCCAAGAAGGTATCTACCAATAGIGICIAIIAGGCAIIIG
ESTD-C7	14 GC	:		ATATCGTGGCCTTA(G/CJTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD-				CTITCATGCACGATAGGCTTTCTCTACTAATCACAGAATTTTGAGAAGAGAGCAAAACAACTTTCAAGG
D4S95	90 T C			ATAATGGGGCAATCACTTTCTTTT/C/CTTCTTTAGAGTCTACCGG
esro-				CT TO THE TOTAL OF THE STAGATOCOTTICACO CARACTERISTICA CONTRA CON
GPPKZL	38 GA		:	AGIC I CAIC I GLOS I SI CANGO I TONO CANGO
ESTID				CTGGGCTCGCCCGCAGCAGCTGCTGGCACCTGGACGCGCGCG
HRASb	82 A'G	:	•	TATTCGTCCACAAAAAGITGCATCTGGATCAGCT
FSTD				CTGGGCTCGCCCCCGCGCTGCTGGCACCTGGACGGCTJGGCGCCCAGGCTCACCTCTATAGTGGGG
HRASa	37 CT	:		TOGTATTOGTOCACAAATGCATCTGGATCAGCT
L COL				GGAGGCAGGAGGTGGGGAGGGGGTCTGTCTGCTCCAGGTCCCACAGAGAGAG
NBAMP	A G	- :	:	TATCCCCACCCCA(AG)TGTGGGCGCTGGGAGTGAAGAGGAGTTGATGCAGGT
	: -			GTGACCTTCTCACTTTAAJAGJAAACTTTACCGGAGAAGAAATTAAATATATATGCTATGGCTATCAGC
OTO CETA	- 0		-	AGATCTGAAATTTAGGATAAAACAGAAAGGAGAGGTATGTAACA
ESIDOIC	0			CCAAGTCGTTCAATTTTAGCTTTGCAGGTTTTAACTIC/TIGATTACTTTTTCTATTCAAATCTCTGTA
ES 136751	0	-	_;	AAATTGAAATATGAACTTAGTTTTCTGATCTATGGTTTCAAGTTAAACAG
	3			CASSTOCA A A COACCTATITIFICA A CONTINA A GAGINA A GAA TOTGIC COCCAA A CTIGIC GCT GAC
				THAT GETT A GO A GOTTTT CACTEGATICATION TO A CACATIAN GITT TACCTTT TIGADADATA
			· · ·	ATCA ACCATT TRANSCENTING SATING
				ALGANGGALI I GACCI GOLI GOCI CONTRACTORI C
EST40562 109 A	109 A			BAIGCOIL IOCULIA MACANATINA CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTR
				GCTCTCTATACCCCTGTGGTCCTCCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGGACTTCACAGAACTGGATGTTGCTGCTGCTGCACTTCACAGAACTGGAATGTGCTGCTGCTGCAAACTTCACAGAACTGGAATGTGCTGCTGCTGCAAACTTCACAGAACTGCAAAAAAAA
				GATTGACAGGTTCATGCAGGCTGTGACAGGATGGAAGACTGGCTGCTCCCTGGUTJGGGAGUCAG
FETTRORE				GTGGACAGCACCCTGGCTTTCAACACCTACGTCCACTTCCAAGGTAAGGCAAACCICICIGGUGGIG
	121CT	:	1	TGGCCCTAGGACTTAGTATCC
ECTOAK				GGGAGTGACAGCTAGAGCACCAAGGGGGGCTICTJTACAGCTGTGTTCTCATGGAGGACAGGCTTCT
168	31 CT	-:-		GCTCATTCTGG
				AATCCCAGCACTTTAGGAGGCTGAGGCAGGCATATCACCAGAGGTCAGGAGTTTGAGACCAGTCTGA
				CCAACATGGTGAAACCCCATCTCTACTAAAAATACAAAATTAGCCAGGCATGGTGGTGCATGCTGT
				AATCCCAGGAGGCTGAGGCAGGAGAATOGCTTGAACCTGGGAGGCCG[AG]AGGTTGTGGTGAGCCGA
ESTD-ALB 180 A G	1801	 	:	GATEGCACCATTGCACTCCAGCCTGGGCAACAAGAGTAAAACTCTGTCTIC

	-			TTCCCGCCAGCCCCCATCCTTGGCACCCTGGTCCCCCTCAGGGGCCCACCCCGCGGCACTCACCGCTCT
				CGCTCTCGGTAACATOCGGCCGGCGCGTCCTTGAGCACATAGCCTGGACCGTTTCCGTATAGGAGG
ES170523	182 G	GT		ACCETETAGECTTCCTETCCGGGGCTTTGCCGGGGCCAGCCTTGGTCGTGGGGGGGG
ESTD-	101		!	CCAGGIGITGIGGCACGIGCCTGIAATCCCAGCTACTCGGGAGACTGAGGCATGAGAATCTTTGAAC CGGGGAGGCGGAGGTTGCAGTGAGCTGACATCQCTJGCCACTGCACTCCAGCCTAGGTGACAGAGC AAGACTCC
707	112.07	-		CAGTGTATCTGGAAAGCCTACAGGACACCAAAATAACCTTAATCATCAATTGGTTACAGGAGGCTTT AAGTTCAGCATCTTTGGCTCACATGAAGGCCAAATTCCGAGAGACJCTJCTAGAAGATTACAGGAGAC CGAATGTATCAAATGGACATCAAGAACTTCAACGATACCTGTCTGGTAGGCCAGGTTTATA GCACACTTGTCAACTTCTGATTGGTGGACTCTGCTGCTAAGAACCT
EST74167 6	137 C			AGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAACAACTGACCCCGGTGGCGGAGGAGAACAACTGACCCCGGTGGCGGAGGAGGAGCTGCAGGCGGCCCCAGGCCCCCGCTGGGCCCCGGAACATGGAGGAACTGCAGGCGGCCCCCAGGCCCCCGCCCCGGCCGG
EST43211	132 C		1	COCCTGGTGCAGTACCGCGGGGGGGGGCCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCG CCTCGCCTCCCACCTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCC TGGCAGTGTACCAGGCCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATCCAGGAGCGCC TGGCAGTGTACCAGGCCGGGGGGCGCGCGCGCGCCCTGGGCCCTCAGCCGCCATCCGCCGCCTGGGGCCCCTGGGGGGCCCCTGGGGGGCCCCTGGGGGG
ESTD- ARSB	126 A		l l	GGAAGAAATGGAGCCTGTGGGAAGGAGGCGTCCGAGGGGTGGGCTTTGTGGCAAGCCCTTGCTGAAGGAGAGCGCTGCTGAAGAAGGAGGGGGGAGGCTCATCATCACAATGGACTGCTGCTGCTGCCAACACCATGAAGAGCTGAAAGGCTGAATGGAAAAGGCTCTGGATGGCTTCGACTGTGGAAAAACCATCATGAAAAGCCTCTGGATGGCTTCGACTGTGGAAAACCATCAGTGAAGCCTGGAATGGCTTGAATATTGACCCAAAC
0770	144 C		i	TGTAGCCAAAGTCACCTCATCATTGGCTGCTGGCAGGCTTGGCCAGTTTGCCAGCTATATCC ATCGAAATGTATTTTCATTGAGAACACCAATATTACAGTTTGTGCTTTCCATTATGAGTCCCAAAAT TCAACCCTCCCGATAGGGCTGGGCCTGACCAAAATATACTGGGTTTCCTGTTTCCTTTTCTGATCAT TCTTACAAGTTATACTCTTATTTGGAAGGCCCTAAAGGCTTATG
EST26021	137 A	37.A	:	TAATGTAAGCTCATCCACCAAGAAGCCTGCACCATGTTTTGAGGTTGAGTGACATGTTCGAAACCTGT CCATAAAGTAATTTTGTGAAAGAAGGAGCAAGAGAACATTCCTCTGCAGCACCTTCACTACCAAATGA GCATTAGCTACTTTTCAGAATTGAAGGAGAAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTTCTTTT
ESTD- BA511	29 4	29 A G	ţ	GGGCAACATAGTGAAACCCCATCTCTACAĮA/GJAAAATACAAAATTAGCCAGGTGTGGTAGCAAG TGCCTGTAGTCCCAGCTACTTGGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTG CAGTGAGCCAAGATGGTGCCACTGCA

				AGCTGGATTATAACTCCTCTTCTTCTGGGGGCCGTGGGGTGGGAGCTGGGGCGAGAGAGTGCCGTT
Eg.				AGATAGTGATGAAGTACATCCATTATAAGCTGTCGCAGAGGGGCTACGAGTGGGATGCGGGAGATGT
	116 A	- :-	:	GEGCEDOSCECCOCOGEGCCCACCEGCATCTTCTCCTCCCA
	2			CAGTGGCTGAGTGGACGATGAGATTCAGAAAOCCATAGAGCCGGAGAGCTCATCATCTGCGCAAGA
		1		GA[CH]CAAAGAGGTCAGCTTCTGTTGTCAGGAAAAGGAACACACATCAGGAACAAAAAAAA
ESTOBCR	69 C I	<u> </u>		AWAILCAMCAICAGGETTAAAAGTGTCTAATAATGTTGAAGACCCCAAAGATCTCATGATAATGATGAAGACCCCAAAGATCTCAAAGATCTTGAAGACCCCAAAGATCTCAAAGATCTTGAAGACCCCAAAGATCTTCAAAGATCTTGAAGACCCCAAAGATCTTCAAAGATCTTGAAGACCCCCAAAGATCTTCAAAAAAATAATAATAATAATAATAATAATAATAA
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			-	TACTGATTATGGCACTCAGGAAAGTATCTCGTTACTGGAAGTTAGCACTCTAGGGAAGGAA
500	- 0	- :	į	GAACCAAATAAAT
-	21	:		ACTA A TETA A GA A A A TET GETA GA GA A A A CTTT GA GA A CATT CAT GT CA C T GA A A GA GA A A CTTT GA GA A CATT CAT GT CA C T GA A A GA GA A A CTTT GA GA A CATT CAT GT CA C T GA A A GA GA A A CTTT GA GA A CATT C A CTT GA A A GA CATT C A CTT GA A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A CTT C A
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BBCA1hb 139 A G	39 <u>A</u>	:	1	GTATTAATGAAA
200	3			ATECATCTCAGGTTTGTTCTGAGACACCTGATGACCTGTTAGATGGTGGAAATAAAGGAAGATAC
				TAGTTTTGCTGAAAATGACATTAAGGAAAGTTCTGCTGTTTTTAGCAAAAGCGTCCAGA[A/G]AGGA
CETT				GAGCTTAGCAGGAGTCCTAGCCCTTTCACCCATACACATTTGGCTCAGGGTTACCGAAGAGGGGCCA
8	126 A.G	:		AGAAATTAGAGTCCTCAGAAGAGAACTTATCTAGTGAGGATGAAGAGCTTCCC
+				ATCCTGAGCTCGCCAATAAGCTTCTTGGTTCTACTTCTCTCCACAAGCCCCCAATTTCACTTTCTCTC
EST51212				GAGGAAATCCCAAGCTTAGGAGCCCTGGAGCCTTTGTGCTCCCACTCAATACAAACAA
	122 A C	-		CTCTACATCT
				ACACAGGTGCTGGCACTGGGGCTGGGGATCCTCCTCCCTJA/GJATTTGCTCCGGGAAGCACALICAL
FSTDC18	404	40 A G		CAA
. '	!			ACACAGGTGCTGGCACTGGGGCTGGGGATCCTCCTCCCCTIA/GJATTTGCTCCGGGAAGCACATICAT
ESTOCIB	404	40 A G	;	CAA
1_				COCAGICAGITTGGGGGACAGCCATGCACTQIACIGCCTCTGGTAGCCTTTCAACCATGCATTCCATC
ECTIVOS	3	31 A C	- 1	TAAGCTCTGCAAAAT
				GTTCCGAATCCTCCTCAAAGTGGCCGGGTTTAATCTGCTCATGACGCTGCGGCTGTGGTCCAGCT
	-			GAGGTGAGGGGCCTTGAAGCTGGGAGTGGGGTTTAGGGACGCGGGTCTCTGCGTGCATGCTCT
EST20118				GAGAGCAAACCTCCCTTGAAGCTGGGAGTGGGGTTTAGGGACGCGGGTCTCTGCGTGCATCCTAAGCT
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1000000	6.7	67 4 5	;	A/G GGATTCAGGAAGGAGGCCACGAGGATCGAAGTTAGTGAAGTC
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				GGCAAGTTTTATTGATAGAGAGAAATCAAATAATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGGATGGACAACAATGGGCAGTGCCAACACATAGGGGTATGAAAAG
ESTD- CB22	119 C T			ACAGGCAAGGAAGGGGTAGAACCATCAAAGGGAA AGGL IGSTGACCCAAAGCAAGGAAGGACACAAGAAAAAAAAAAAA
				TAGNACCATCAAAGAAGAATAGGCTGGTGACCCCAAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCATTATGGTCCTTTCCCGGCCTTCTCTCACACATACACAGAGCCCCTACCAGGACCAGACAGA
			•	CTCAGAGCAACCCTAGCCCCATTACCTCTTCCCTTTCCAGAGGACCTGAAAACGTGTTCCCACCCGA
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CB24	145 A	11		GAAGGAGGTGCACAGTCAGCACAGACCGCAGCCCTCAAGGAG
				GTTTTCTTTCAGACTGTGGCTTCACCTCCGGTAAGTGAGTCTCTCCTTTTTCTCTCTATCTTTCGCCGTC
				TOTGCTCTCGAACCAGGCCATGGAGAATCCACGGACACAGGGGGGGG
ESTD	_			TGCACAGGT[A/G]CCTACATGCTCTGTTCTTGTCAACAGAGTCTTACCAGCAAGGGGTCCTGTCTGCC
CB25	146 A			ACCATCCTCTATGAGATCTTGCTAGGGAAGGCCACCTTGTATGCCGTG
				TTTTCTGTTTCCCTGAAGATTGAGCTCCCAACCCCCAAGTACGAAATAGGCTAAACCAATAAAAAT
				TGTGTGTTGGGCCTGGTTGCATTTCAGGAGTGTCTGTGGAGTTCTGCTCATCACTGACJCATJATCTTC
ESTO				TGATTTAGGGAAAGCAGCATTCCCTTGGACATCTGAAGTGACAGCCCTCTTTCTCTCTC
CB27	125 CT			GCTTTCTCCTGTTCATCCTGATGGAAGTCCTCAAACACCCATTTCCATACC
	-			TTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATAGGCAGGTATATGA(A/T)ATGTA
				TTTCTTAAACAATAAACTTGAAAGTCCAAAATTACTCCTTGATCCATGGACTGCAGAATAAATGTTA
ESTD				TTTTAGCTGTCAGAAAAAAATACTAATCTTGCATATGTTCATCAGAGCCCTTGGGTGACCAGGTGIA
D4S338	59 A T			TIGCCAATAAGCAGTAATATTTTGAGGGAATCTTGTTTTCAATGCAGTAG
ESTO				CAGGCCAGCGTGGTGGTGGTCACCATCCCGGCAGAAACAGGTCAGCCACCACTATGGA/GJCA
CYP2D6	61 A	::	***	GGTTCTCATCATTGAAGCTGCTCTCAGGGTTCCCCTTGGCCTGAGCAGGGCCGAGAGGATACTUGG
				AAAAAAACATTTTAACACCTTTTCAATCATATACACCATAAACATTTCCATTTTCACATAAGTCA
				GTTTGAGCTGAGTTTTCCAATTACTTGCAATCTAAAATGTCATAACTGATTAATGCAAGTTCAACAG
ESTO				ACAACTTTCCCAAGCATCTACGATCAGAAAGGTGAAATATTACATATCTGGATTAAATTATGCCCA
D11S1873	40 A		:	TATCTGCATGTC
				CATCCCCAAGCCCATCCTTAGCCACTGGCATTTTTGCCGCCTCTGACAGATACACTCAGGGCCGT
				CATGCTGCACACATOCAGGGGGGGCGCCTACCTTTGTAGTCCATGGGAAAGGCTCCTCTGGGGGGGG
53				GGGTTGTGTGGCTATGTGGTGGTCTTGTGTAGA[CTJGGGGGCTTTGGTTTCAGTTGCACTATTGCGTT
D17S33b 169 CT	169 C		::	ATTGCAGATTGCTTTGTCTTTCCACCTGAGCGAGCCTC

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	_			CAICCCAAGCCAICLINGSCALCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
	_			CATGCTGCTJACACATCCAGGGGGGCGCCTACCCTTGTAGTCCATGGGGGGGG
FSTD				GTGGGGTTGTGTGGCTATGTGGTGGTCTTGTGTAGACGGCGCTTTGGTTTCAGTTGCACTATTGCTT
iga iga	75 CT	:	:	ATTGCAGATTGCTTTCCACCTGAGCGAGCCTC
÷				TTTGAGACCACCTGGCCAACATGGCGAAATCACATCTCTACCAAAATTACAAAATTAGCTGGGTGT
	_			GGIGGIACAIGCCIAICGIAATOCCAGCIACAICGGGAGGCTGAGGCAGGAGAATTGCTTGAACCC(A
Esto				/GJGGAGGCAGAGCTTGCAGTGAGCCAAGATCACACCACTGCACTTACAGOCTGGGTGACACAGTGGA
_	133 A			GACTCTGTCTCAA
				AACTGATTAGAACCTGAAAATACATATTTTATCTGAAAAAGTCGAGTTATTGGCTCATCACATTGG
				AATTITTGCATCATTAAAAATCCAATAAAGTACACTGTAATAAAGAATTTAACAGAATATCATTGI
ESTD				TTATICAAACTATTTATCACTTATTTATTGGTAAGCCATACTAAATTCTAAAGCATGTTTCTGAAAG
03511	44			TITA
				AGGITCCACATTAITGCTGATGTTTGCTGATGTTTCQAGGGGAGCCTTGATGTCATTCTGTATCTCCT
ESTID				CAGGTATCCCACCTTGAGACGTACTTTTCAAAACTCTCTACAGCCGTTGTTGTTATTAATTCAAGGT
03812	37 A G	:	;	TGAACATAAAGTA
				GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCCTGC
				TGAGICTTATTCAAAACTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTCCC
cem		-		AGAAGTGAAACATACTGCTCCTAGAAGCCAGAGTCATACTGGATGTTCTGTTTCGGTCTTCACGATGG
	247 CT	:	;	CAGGTATGAAATATAATCTGTCCTTTATTTGGAAGGATGGCTTGGT
				GATCATGTGGCCCAAGTGGCAGAGGTACTTATACCATGACCAGACCTGCTAGCAGAACATTTCCTGC
	_			TGAGTCTTATTCAAAACTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTCCC
ESTD				AGAAGTGAAACATACTGCTCCTAQAAGCCAGAGTCATACTGGATGTTCTGTTTCGGTCTTCACGATGG
	248 G	9	1	CAGGTATGAAATATAATCTGTCCTTTATTTGGAAGGATGCCGGTATGT
Γ				TGAATCTTAATTGCTATCTCTACAAAATGTATAAATCCTGAATCTGACATCTAGCCACCTCCATAGAT
ESTIP				AACTGCTAGAGACCCJAGIGTCTCCTACATCATCCTTTCACAAACATTTTCATCCATGGACTCCATAC
078399	B3 A G	···	1	TAGAATATTTGAAGAACAACATGACAAACATTTTC
				GTGGGGACACOGAGGGCTCCAGGCTGGCACGTTGCACGTGTGGCTCAAGCAGCTGCTCGGCCTCCACT
				TOCATGGGTGTGGGGGCCTGGGGACCTCACTGTCCCTGGGGGAGGGA
				GAATGCTGATT[ACJTCTGGTGGAGAACCAGAACTTCTGGCCTGTGGGTAGGGGCAGCTGCTTCCAAG
ESTD-DMb 146 A	146 A	-:-	:	ACCTCCTGATTTGAGGAAGGGGAGCAGAGGGAAGAGAGAAGAGAGT
				GTGGGGACACCGAGGGTTCCAGGCTGGGCCTTGCACGTGTGGGCTCAAGCAGCTGCTCGGCCTCCAAC
				GITTCCATGGGTGTGGGGCCTGGGACCTCACTGTCCCTGGGGAGGAGGAGGGAG
	_			CAGAATGCTGATTATCTGGTGGAGAACCAGAACTTCTGGCCTGTGGGTAGGGGCAGCTGCTTCCAAGA
FSTD-DMa 66 CIG	999	<u>ි</u>	:	CCTCCTGATTTGAGGAAGGGGAGCAGAGAGCGAAGAGAGAG

FSTD			. TOCOCAGCOCTATOGGTCATATTGGACTATGACACTGACGTCTCTGGAGAGATCCACACACA
	154 CT	1	AGAGGAGATTGCTCTGGGGGCTTTCGCTATTAAGAAACTAAGGTAC
i			TCTGCCTTTGGTGCAGGAGGCTGCCCGGCGAGCCCAGGAGCTGGAGATGGAGATGCTCCCAACCA
			GCCCACCCGAGGGACCCGGTACAGCCCCATCCCCAGCCACCCAC
ESTD-		_	TCCCACCACGGTCTCCACAGCACTCCCGACAGCCCCACAAACCCACAGAACAAAAAAAA
DRD2	144 C		ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAAATG
			AAGACGATGGCCAGGATGAGCGCGCAGTAGGAGGGCATAGTAGTAGGCATGTGGGCGGGC
ESTD		· ———	CACCTGTGGAGTTCTCTGCCCCACAGGTGTAGTTCAGGTGGQQTALCAGACTGGCTCAGAGATGCC
	109 CT		ATAGCOCAGAGGGAGGTGCGTGATGCGAGGGGGTTTCCTGTGAGGAGA
			TCTTTCAGGATCCGCATCTGCGCCTGGTTGGGCATCGCTCCGCTAGGTGTCAGCGGCTCCACCAGCTGG
ESTD			GETEAGGGGGTGGTGGGTCAGTGGCTJGGGGGCCGGTGCAGACCCCACGCGGGGCTGGGAAGAUTTCA
	93 CT		OCCCGCCTCACCTCCGTTTCCTGCAGCAGTCTCCGCATCGTGTACT
÷ ·			ACTCACAGTGCTTTTAAGTGAAAATGGTCGAGAAAGAGGCACC(A/G)GGAAGCCGTCCTGGCGCCTG
			GCAGTOCGTGGGACGGGATGGTTCTGGCTGTTTGAGATTCTCAAAGGAGCGAGC
Cern			CACAGACTATTTTAGATTTTCTTTTGCCTTTTGCAACCAGGAACAGCAAATGCAAAAACTCTTTGAG
2 62	43 A G	;	AGGGTAGGAGGGAAGGAAACAACCATGTCATTTCAGAAGTTAGTT
3			AGATCCTGATGATTTTTTTCCTATTTTTTCTAAATGTTTTACAGTTTGAAGTTTTAGATTTATGCCCA
			TGCTCCATTITIGAGITAATATTITGTGTAAAGTATGATGTTTA(AGGTCAAACTICATTITTITTICC
ESTD-F9	111 A G	<u>.</u>	ATAGGTATGTCCAATTTATCCAGCACAATTTGTTAAAACAAAAAAC
			CTTCCTATGGGATTTGACTTTATTTTCTCCATTGTCTTACCTTTTACAGGTGTTAATATAGTGAAAAG
			GAAGCTTGCAGCTCATGACAATTTGAAGCTGACAATTACACAAGGAAGG
ECT68787		-	AGAATCAAGCACTTTTCGAAACATTGAAGTTGTTTTTGAACTTGGTGTCACCTTTAATTACAACCTAG
	144 A	1	CAGACGGAACTGAACTCAGGGTAAGAAT
			CGCAGACCGGTCAGTGTGGGGGTCGGGGGGGGGAAGGGGGGGG
			TTCCGGGGTGACTTTCCCGTTCTGTGCTTGCAGAGAGGCGGGGAGAACACAGAGGCCAACTGGCTAA
ESTID			GTGTAAGGGACCTCTGGTCGCACCGTGTTCTGCTGCCCCTGTTCAGCTGTCTGT
_	200 C.G	:	GIGACTCTGTCCCGGAAATTCCGAGAGCT
-			GTTTTATGCATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCCACTCCTGGTCACCATGAC
			AACCACAGGCCCTCTCAGGAJAGCACAGTAAGCCCTGGCAGGAGAATCCCCCACCCCA
			TGGAGCAGGAAATGCCGAGCGCCCTGAGCCCCAGGGAAGCAGGCIAGGAIGIGAGAGAACAACAA
ESTOGCK	88;AG	:	ACCTGCAGCCTAATTACTCAAAAGCTGTCCCCAGGTCACAG

			GTGGGGGCAACAGTGGGAGGAGAAAAGGGGCTATAAAAGGGGCCCACAAGAGGAGUGGULIVII
EST34088			AGGATCCCAAGGCCCAACTCCCCGAAGCACTCAGGGTCCTGTGGAACAGCTCACCTAACTCCTAACTCCCAAGTCCCCAAGTCCCCAAGTCCAAGTCCCCAAGTCCAAGTCCCCAAGTCCAAGTCCCCAAGTCCAAGTCCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAA
	62 A.T	:	ACAGGTAAG
esno			GACCCTGAGTACCTCCCTAGTGAGCAAGATGTGCTCCGGTCCAGGGTCAAAACCACAAGGGGCATCA
GNAT2	56 A G	;	TTGAAACCAAGTTTTCCGTCAAAGACTTGAATTTCAGGIAAGIGCAIGGIICCUIAGG
			GGGCTAAAATTTCCGAGCAACTTTGCATAGACTGTTTTATTTGACTTGACAGGATTGCTAGAGATAGG
		-	CAGGGAGAGGAAGATGTGTTACAGTTTGTCAGAGAATAAAAAGGATAACCTGGGGTTTTCTGTGC
			TTTGCTTCTTCACATCCCTGGGGAGTTAATAGCTGCAATTTTTCAAAGAACGGTATACAGGGACAGCA
ESTD-HT2 154 G	546	;	AAGCGCAGTCGTGAAGTTTTCAAACAAGACACCCTT
2			AACACAAGCCCCAGCGAGAATTGAACTCGCGACCCCTGGTTTACAAGACCAGTGCTCTAACCCT
			GAGCIATGGAGCCCTCGTCTGCTGTTGGTTTTCTTCCTTTCATCTTATAGATTGATGTTATGCTCCTA
			GCATTCCGGCTACCGAATAGGATGTTAGCTTGAGTAAAATTCCAGGATATTCTCCTACAAAATGAAA
FETT-HTS 149 C	149	:	ACATTITICGTGCTCTGTAAATCCCTCGAAAAGGTTCT
-			CTGAGAAACAATTGGCAAAATAAAGGAATTTGGCACTCCCCACCCCCTCTTCTCTTCTCTCTC
1			CITTGAGTCAAATTGGCCTGGACTTGAGTCCCTGAACCAGCAAAGAAAAAAAGAAGGAAG
E513/382		;	AATCACAGGTGGGCACGTCGCGTCTACCGCCATCTCCCCTTCTCACGGGAATTTTCAGGGTAAACT
		·	ACCCAGTGGAGCCCGCTCATTGCACGGTCTTGGCAGGAGGTGCJCTJCTGGGAGGAGGAGGAGGATG
2 685	43 CT	<u>:</u>	TTCCAGGGCACACATAGCTTAGTGGAGCTC
<u> </u>		:	TTTACTATTTCAATGGATACAGAATTGTGGGAGTCACTATATTCCTATGAACAAAAATTCAGATTT
			CAGTGTTAAGTAATGTTGCCTACATTGTGTGAGTGACGGGGCAGTGGTGGATCCGAGAGTGTGGTGGT
-			TGCACGACATAATGATTCAGAAAGCAATATGGAAAGATGAGTATCTATGGATACGAACTGAAAGT
4 2 2 2	12001		ATGTAAATACTTCACAAAATACTAATAAACGGAGTTGAATATAAAAACCCA
2			CAAAGTAAGCACCCAATAAATGTTAGCTATTACTATCATTATTATTATTTTTATTTTTATTTTTTT
			AGATGGAGTCTGGCTCTGTCACCCAGGCTGGAGTGCAGTGGGAAGCATCTCGGCTCACTGCAAGCI
			CTGOCTOCTGGGTTCATGCCATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGAATACAGGCACCACC
ESTO-11	ESTO-18 14 1 10 A G	<u>:</u>	ACTETTCCCGGCTAATTTTTTTTTTTTTAGTAGAGCGGAGTTCACCGT
			CCACTTACAGATGGATAAATGGGTACAATGAAGGGCCAATAGCCCTCCCT
ESTD-IL 18	99 A G		GGGTCTCTACCTTGGGTGCTGTTCTCTGCCTC/AGGGGAGCTCTCTGTCAAI I GCAGG
			TOCAGGGTGGCTGGACCCCAGGCCCCAGCTCTGCAGGAGGAGGACGTGGCTGGGCTGGTGAGCAIG
			TGGGGGTGAGCCCAGGGGCCCCAAGGCAGGCACCTGGCCTTCAGCCTGCCT
			TOCCAGATCACTGTCCTTCTGCCATGGCCCTGTGGATGCGCCTCCTGCCTG
FST74082	EST74082 134 ATT	:	CTCTGGGGGACCTGACCCAGCCGTGGGAACCAACACCTGGGGGACCAACACCTGGGGGACCAACACCTGGGGGACCAACACCTGGGGAACCAACACCTGGGAACCAACACCTGGGAACCAACACCTGGGAACCAACACCTGGGAACCAACACCTGGGAACCAACACCTGGGAACCAACACCTGGGAACCAACACCTGGGAACCAACACCTGGGAACCAACACCTGGGAACCAACACCTGGGAACCAACACCTGGAACACACAC

			······································	GCCCTCCTCTTCCAATTCTGTCCCTATAGTTTTCCTCTATTAAGTGAACTACATGCATTCTTTAGT GGATAGATGCACACAAACACACAGAGCCATTATGGGGAAGGATCCACGTGTGGGCCATATTGTAACA
EST45311 0	151 CT			CATTITICIGCAAATIC/TACCICTITICATTAACAGCCCTTATTCAATGGCCTTTTCTTTT
			,	TGCCCCATCACGCGGCCGAGACATGGCTTGCCACAGCTCTTGAGGATGTCACCAATTAACCAGAAATCCCAGTTATTTTCQAAQCCTCAAAATGACAGCCATGGCCGGCCGGCGGGGTGCTTCTGGGGGCTCGTCGGG
EST65258	- C			GGGACAGCTCCACTCTGACTGGCACAGTCTTTGCATGGAGACTTGAGGAGGGAG
EST38216	200			ATGCAGGATGAAGGTGGACAGGGAGGATJGAGGCCCAACCTGTCATCCCAGGGCCTGCAGATGTCG
က	26 A T			CTGGACTATGGGTTTGTGACCCCACTGACCTCCATGAGCATCAGGG
				ATACTAGTACAAGTGGTAATTTTTGTACATTACACTAAATTATTAGCATTTGTTTTAGCATTACCTAA
				TITITICCTGCTCCATGCAGACTGTTAGCTTTTACCTTAAATGCTTATTTAAAATGACAGTGGAAG
				TITITITICCTC G/TJAAGTGCCAGTATTCCCAGAGTTTTGGTTTTTGAACTAGCAATGCCTGTGAA
EST62782 149 GT		1		AAAGAAACTGAATACCTAAGATTTCTGTCTTGGGGTTTTTGGTGCATGCA
				CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTTACCTTTTTGGCAATATT
				AAAGGAAGAAAATGCATTTTAAAGTAACTGCTAAGGTTTTTTCCATTAAACCACTATTACTTCTAAG
				AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGIC/IJTGCTTTTTAAATAGT
KRT10b	183 CT	:		CTCTGCCCAGATACATCTCCCCTATATAAGTTATAACCAGTATIGATA
				CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTTACCTTTTTGGCAATATT
				AAAGGAAGAAAATGCATTTTAAAGTAACTGCTAAGGTTTTTTCCATTAAACCACTATTACTTCTA(A)
ESTO				GIGAGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTTAAATAGTC
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		• •	CATCTCCTCCATGAAGAGCACAGAGAGTTATTTATTCCTGAAGTCCGGATCTATGACTCAGGGACAI
EST71770			ATAAATGTACTGTGATTGTGAACAACAAGAGAAAAGCGACAGGCAGG
	189 CG		AGGAGTGCCCAGTCCCAGGGTGACACTGGACAAGAAGAGGGCCATCCAAGG
			TTCCTGCATCCTGTCTGGAAGTTAGAAGGAAACAGACCACAGACCTGGTCCCCAAAAGAAATGGAGG
			CAATAGGTTTTGAGGGGCATGAGGACGGGGTTCAGCCTCCAGGGTCCTACACACAAATCAGTCAG
EGIL			GCCCAGAAGACCCCCCTC[A/G]GAATCGGAGCAGGGAGGGATGGGGGAGTGTGAGGGGTATCCTTGATG
	52 A G	<u>:</u>	CTTGTGTGTCCCAACTTTCCAAATCCCCGCCCCCGCGATGG
-			TTCCTGCTGCTGTGTGGAAGTTAGAAGGAAACAGACACACAGACCTGGTCCCCAAAAGAAATGGAGG
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£			GCCCAGAAGACCCCCTCAGAATCGGAGCAGGAGGATGGGGAGTGTGAGGGGTATCCTTGATGCTT
TNEA		-:	GTGTGTCCCCAACTTTCCAAATCCCCGCGCGATGG
+	7		CAAATTACAGGGTCAACTGCTATGATGTTTTGGAGCCCAGTCACCCTTTGGTGGCTACAAGATGTCG
EST52418			GGGAGTGGCCGGGAGTTGGGCGAGTACGGGCTGCAGGCATACACTĮA/GJAAGTGAAAACTGTGAGTG
	113 A.G		991
			CCCACTCTATTTGCCCAGCCCAGGGACAGAGCTGATCCTTGAACTCTTAAGTTCCACATTGCCAGGA
			CCAGTGAGCAGCAACAGGGGCGAAGJGGGGCTGGCTTATCAGCCTCCCAGCCCAG
EST13586			CATAAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGAACTGCGAGAAGGAGGAGGIGUGIUUIGUIGUIGUU
6	89 A G	:	COGGICACTC
,	\vdash		AGGCAGAAACTGGGCCCCCATGCGGGGGGCGTGGAAGGCCACTTGAGCTTCCTGGAGAAGGACCTGA
			GGGACAAGGICAACTCCTTCTTCAGCACCTTCAAGGAGAAAGAGGGCCAGGACAAG(A/T)CTCTC
FCT51976			OCTCCCTGAGCTGGAGCAACAGCAGGAACAGCAGCAGCAGCAGCAGCAGGAGCAGGTGCAGATGCTG
7	23 A T	<u> </u>	GCCCCTTTGGAGGCTGAGCTGCCCCTGGTGC
			CCACTTTGGTAGTGCCAGTGTGACTCATCACAATGATTTCTCCAGTGCTCATCTTGTTCTCGAGTTTT
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EST11458			CCCIA/GITTAAAAACATTCTATGAGCCAGGAGAAGAGATTACGTATICCIGCAAGCCGGGGCTATGT
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112	 S		TGGCAATAT
			AGTGACTTCCAAGGAAATGGCTACCCAACTTGCCTTCATGCGCCTGCTGGCCAACTATGCCTCTCAGA
			ACATCACCTACCACTGCAAGAACAGCATTGCATACATGGATGAGGAGACTGGJAACCTGAAAA
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					GCAGGTAAACTGTGGTTCACAACGTATTGTTCTTTCATAAAGAAAG
EST16183		_			AGGAAGGCACTGTCTTCCTGGCCCTTCTTCGTTCATATTTTATGTCACTGTCCTAACGTGGGCCG1G1
2b	59 A G	2			GCAAGAGATCTTTGAGA
EST16198		F			AATCTTAGGCTCTTGGCTTTCAAAATCA(G/A)TACAGACAGATAAGAGCTTTAAGTATTTCGCATTT
48	28 GA	4		•••	CCCCAGAGGAAAAGTCAGCATCATAAACCACATGGGTCACATGCTCACGCACATGGTGTC
EST16229	\vdash	Γ			TGTGAACTCGAATTCGCTTGTCCAAGTCCTGAGTCACAGTTTCATTTGGGAGTTCJCCTGTGCAGCC
2c	52 T C	0			CTTGCCAGTTTCCACGAGGCAGGATACTCCACTAGCTGATTCAGACAGGCAGAGGGCTGCA
EST16229					TGTGAACTCGAATTCGCTTGTCCAAGTCCTGAGTCACAGTTTCATTTCJTGGGAGTCCCTGTGCAGCC
2b	45 T C	근		:	CTTGCCAGTTTCCACGAGGCAGGATACTCCACTAGCTGATTCAGACAGGCAGAGGCTGCA
					CAGACTTTICCTCACACCTCATTGGCTGGAACTGGGTCACATGCACATCCTTGAACTATCATTGGCAA
			GGAGCCATTGT	GCCTAGATTTT	GGAGCCATTGT GCCTAGATTTT AGGGAAATGGGTCATCAAAATTGCTTAAGGCCAAGCAGGAGCCATTGTTGGGGGTTA(A/GJACTGTCC
WI-16816	124	<u>A</u>	WI-16816 124 A G TGGGGTTA	GTTCAGGACAG	GTTCAGGACAG TGAACAAAATCTAGGCTC
	\vdash	├-			GCCACTCTCCTGTGGCTTGCTCCTGTCCAGCTGCTGTCCCAGTGCCACA[G/A]TGGTCTAGCCTCATGG
EST16269		_			CAGAAGCATTTTAGCCAACTCCTGGTCTGCTCCACTCTCTTCCTTC
25	49 GA	_ <u>কু</u>			TCTTCCTCCAATC
		\vdash			GTCACCCCAGCCAATGCTTCAGGAATAAATGATGGTGCTGCAGCTGTTGTTCTTATGAAGAAGTCAG
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16824b	83 GA	. ডু	;		GCCTTCCATTATGGGAATA
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CETTEAAR		 			TIGCITITATTAATCCAGAACGGCATGCTACAGATACTGTACAGCATGAACATTTATTCATTACAAA
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		GAAAATGCCA	GACACATGTCA	GAAAATGCCA GACACATGTCA ACATGAATGGCAACCTCTTAGGTGGGAGAAGACAATTCTCCCCCTTTCACCCAAAGGTTACTCTGAC
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WI-16910	74 GAAA	AAA	TAACAGA	CTAGAA[G/A]GTATCTGTTATAGAAACGATACTTCATTTTGGGCCTGAACCAGTGAAGGT
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WI-	108	- C		AATCAGAAGCAGTCAGTGGCCCCGTGGTTTCCAGACGGCT[TICJTCTTTGTTAAGAAATTA
			TTGTATTATAA	TTGTATTATAA AGCGTCCAACAGATGTTTCCATCAAGGACTTTGTTTTTTCGTCTTCTTCTTCTTGTTTTATAATAC
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		CATTICITIES		GAAATCGAATACGTCCATTTCTTTGTAAAATAACAATAACGTT[A/GJAAGGCAAAAGCAAGATTCTG
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İ	<u> </u>	-			TCATGGACATOCTGAAGCAGACACAAAATATAGAGAATCCTGCACTTOCCAAGTCTGGTGGCACAG GCTTCAACAATTACJC/GJAACATCTTGCCCATTTTGTTTCATTATCGGCACCACACTGACAGATGAG
17180b	8	81 CG			GGAGTC
			CACAAAAATA		TCATGGACATCCTGAAGCAGACACAAAATATAGAGAATCCTGCACTTT/CJCCCAAGTCTCGCA
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17180a	47	7	47 T C TGCA	ПССС	GGAGTC
			TGTTCTCTAAA CAAGAAATAT	CAAGAAATAT	TGAGGTAGCAGGCATTCTTAAGAAATGTTCTCTAAACTTTAGATATCTCCCATGGCTTCCACAGA
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WI-17156	54	0	54 GCTCCCA	TGTGGAA	TAATATTCTTG
Š		i			CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAACATCTCATGCACGTGCGTG
17149b	79	79 T C			ACCCAATTGTCA[T/C]GTGTATGAACTACAAAAGGATGGGGAAAAGAACACATTTCCTCACA
Š			AGGTTTGA	CCACGCACGTG	CCACGCACGTG CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAGGAACATCGGTCATGCAGGCGGGAGAAGGAACATCGGTCATGCAGGGGAGAAGGAAG
17149a	48	0	48 C G AGGAGGAACA CATGA		GAAACCCAATTGTCATGTGTATGAACTACAAAAGGATGGGGAAAAGAACACALITICUTCACA
			GCAGAAGTAG	GGTGAGGTGGT	GCAGAAGTAG GGTGAGGTGGT ATTTTGCTATGTTGCCTGGGCTGGACTCCAGCAATCCTCCTGCCTCAGCAGAAGTAGCTGGGGCTAGG
WI-17197		<u>8</u>	67 GA CTGGGGCTAC GCATACC		/AIGGTATGCACCACCTCACCCTGCTTATCAGTTTCGTTTAAIAGAATATTGACTTTTAAATGCACA
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			тоссеттетс	TCCATTTGTCC	TOCCOCTTGTC TCCATTTGTCC ACCATCTCTGTTTGAATTTGAATACACAGATACATGCAAGATATGTTACAAGAAACAATGCAAGAAACAATGCAAGAAACAATGCA
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TGP.				ACAAGTTCAAAAGGAQACTTCCTTTGTTTTAATGCAGCTGTGCTCAGAAGCCTGTGATTTCCTAGGA AACCATCTGGGTTTAGCCCATTAGAAAAATGCAGTTTAAAGCAGTGTCAGCIGACTGGCTGAC
A003P30	117 0		1,	GGTACCCTTGGAGATACT
		CCAAACCTCC	TGTAAACAGCT	GCTTGTCTTTATGTTTAGGTTCGGGGGAAAGGAAGGGCTGACAACCGCAACCAGCAGACATCTGGACACCCAGCCCAACCAGCAGACATCGACAACAGCT AAGGGTCAGGAGAGGTTTGCAGAACTTCTTTGTCTTGGCTAACAGGTGTGTGATGTGACAATAGCCA
TIGH- A004S34	156 CT A	CATTCCTATA	A AACTGTTTTG	CATTCCTATAA AACTGTTTTG AACCTCCTCATTCCTATAAA C/T]CTTTAACAAAAACAGTTAGCTGTTTACAAAACAGTTAGCTGTT A
Tree.				AACAACAGTGTAATCTTTAACAGGGGATGTTAAAGGTAAGAAGGTCAGGAAGATGAAACCAAAATGATGAGAAAACCTATAAATGAAAAACCATGGCGATTIYCIAAATAGAAAACCTATAAATGAAAAAGCA
A004T44b	97 A C	d		GGTCTGGACTTAGCAAAGAACAATATGACTTAGCAAAGAAACAATATAG
		GGAAGATAAA		AACAACAGTGTAATCTTTAACAGGGGATGTTAAAGGTAAGAAGTCAGGAAGATAAACCAAAATGAT
TIGR.		CCAAAATGAT	GCCATGCAAAA	CCAAAATGAT GCCATGCAAAA TGAGAJTATGATAAAGAATTTTGCATGGCGATTAAAATAGAAAAACCTATAAATGTAGAAAAAGCA
A004T44a	- 1	69 G A TGA	TICITIALCA	GGICIGGACIIAGCAAAGAAACAAIIAIGACIIAGCAAAGAAACAAIAIG
				CCTACAATCCTATAATATTGCAAGGGTTGGGAAGGATGCAGGAAAACAGGCATTCTCTTA[7/C]GCC
TGR		CAGGAAAACA	TCCTTCCCACA	CAGGAAAACA TCCTTCCCACA TTTTGTGGGAAGGATCAATTGGGTGCATGCACTTTAGGGGACAATTTGGGCAGTAGCTGTCAATTTC
A004V08		60 T C GGCATTCTCTT AAAGGC	T AAAGGC	AGTAGCTGTCAAATTTCAAA
				TCTAGCTATAAGACCAGATTTTAATATTCTAGATATAGAATTATCCAGAATAATTCTATTGAATTGA
TGA.				CTGATTACAAAATGTTAACAGCTGGATAAACGGTAAAATATGCATTATCTTCACATGA[A/G]AAGGT
A004V26		125 A G		TTCAGTTTATAAATGCTTAAATACTGTATCTATTTGCTTAAATACTGTATCTATTGG
1GP				CCAGGCTATAATGTTGTGGGTGCGATCTC(A/G)GCTCACTGCAACCTCCGCCTCCCAGGTTCAAGCAA
A004V28		теттетеест	3 CGGAGGTTGCA	tettetegete oggagetteca itetecteceteageetetteagragoggaltagaetegegactacaggeaooggegacegecacegaceacetaaltitig
, as		29 A G CGATCTC	GTGAGC	TATTITITAGTAGAGATTGTATTTTTAGTAGAGACAGG
				TAAGTITTCCTTCTTCTGTAGGA[T/C]GTCTCCATGTTACAGTCAACTATAAAACATGGCTCATGT
		AAGTTTTCCT	ттттатавтте	AAGTTITCCTI TTTTATAGTTG TCACTCTGGGCTTCGCTTCAGAGGAGTTTGATATTTTGGAAGTGGTACCTTTGTCTGTGTGCTTTCA
HG.F.		CTCTTCTGTAC	3 ACTGTAACATG	CTCTTCTGTAG ACTGTAACATG GACCAACGCTTCTTTCATTTCTTCAAGGGTTCCTTCCAAAGGAGTTAAATCATCATCATGTCCAATC
A004X20		25 T C GA	GAGAC	ATCATCATGTCCTT
		TTTGAAATCT	TITCTITATEGA	TTTGAAATCTT TTCTTTATGGA TTTTGAAATCTTAGAGTAGAACCCACTT/CJACTCTAGTAATACTTGTAATAAAATTAAAATAGTTTT
1GB		AGAGTAGAAC	: AGTGTTTAAAA	AGAGTAGAAC AGTGTTTAAAA AAACACTTCCATAAAGAATTAGGGGTGCCCAGCTCCTTGATTTCCCCCTAGGGATAAAGATATCCAT
A004X30		26 T C CCAC	СТАТТТ	GTTAGGGATAAAGATATCCATGTAC
				CACGGTATATGCCTTATATATGGTATATATACAGATCGTACACAATATATTTAACAGTTTGACATG
			CTTATAATTAG	CTTATAATTAG GGGTCCACAGTACCTTCATTTGGGTATGCAAAACT[T]/GJTTGCTTTCATGAAATTTCTAATTATAAGG
nga.		TICATITGGG	T AAATTTCATGA	TICATTIGGGT AAATTICATGA ACTGTTGCTTTCTTCATATGGACATTATACAAAAATACAGTCTCTTTAGTGATTTAAGACGTC
A004Z04	102	A004Z04 102TTGATGCAAAACT AAGCAA	r AAGCAA	TCTTTAGTGATTTAAGACTG

	<u> </u>				TAAGTGGAGACAAGTTTATTGGAGGAGCTTGACACCCCTCTTCTGCCTAGCTTGAGAGAACAACTGC
Ę,		_ <u>ŏ</u>	GAACAACT (AAGATGGTCAT	GAGAACAACT AAGATGGTCAT AGCATTTTTTTTTTTTT
A004Z19	85,C	1 60	85,CT GCAGCATTTT CGGGAAGA		TCCCATATCGCTGTCTTTAGTGAGACTGAGGATCTGGTATAAGGAAACAGATC
	<u> </u>			-	GTCTTAGCAGAGGAGATAACTTTGAGGGACAGOCOCCAAGGCGCCCAGGTAGOCTTCAGGGGGCGGGCA
TGP.		<u>1</u>	GGGGAGGT	CAGGGCTGCCG	TTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
A004Z42c	89	TAGG	89 CT AGGAGACT	2015	CATCATCTGTGTCTTC
HCPL					TATGGACTGTGTAGAATATGATTTGGACAAGAAGGGTATGATCTAATAGTAATAGACTGAGAGGGG
A005D17	-	_			AAACCCAGCAAGGCIT/CJGTCTAGATTCTTCTTGGCCTCTCTGTGCAGGATTCCTTCTTGGGCACAC
	8	81 T C			GGGGTGGGACCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAACAC
- H	!	-	1	GAGAGGCCAA	GAGAGGCCAA TATGGACTGTGTAGAAATATGATTTGGACAAGAAGGGTATGATCTAATAGTAATAGACTGAGAGGGG
4005017		<u> </u>	GGGGAAACCC	GAAGAATCTAG	GAAGAATCTAG AAACCCAGCAAGGGC CTGTCTAGATTCTTGGCCTCTGTGCAGGATTCCTTCCTTC
2	790	79 GICIAGCAAG	CAAG	ĄÇ	GGGGTGGGACCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAACAC
		F	PACATTATT	TTGTCTATTAT	TTABCATTATT TTGICTATTAT CATCAGTAACATATACACAATTGGTCATCAACTGAACTTTGCCTCCAATATATTTCTATACAATACTT
900		٠	ACTTABAA	TTAAAGCCAAC	GAACTTAAAA TTAAAGCCAAC AACATTATTGAACTTAAAAACTGTTACACT[G/I]TTTGTTGGCTTTAAATAATAATAAGACAATGATTTTG
A005044	97	L C	97 GT CTGTTACAC	AAAA	TCTATTACTTAGTGATAGACAAAGTGATTACTTTGTTAGACAAAGTGATTACTTTGTTAC
10000	5		Г		GEAGTTCAAATTTATAACCAGGCCTCTIG/AICTCACAGCTGTACTGGCTAGGCAAAGCTTTCCAGAC
00					ACAAAGCCACCTGCCTGCCATGTGGATAGTACTCTTTGCCTGCTTGCCCCTACAAAGCCACCTTCTAT
A005F31b		27 G A		:	TTCATACCAATACCTTCTATTTCATACCAATAAG
2000	!	-	:		
					CTCAGTGTAAAAACTTTGTTTAGGGAAAAAAAAAAAAAA
100					OCAGGCTGGATGGTGCTGAGACAGAATGACCCCTTGGGCTCCTTTATTTTGTTCTTTTCAACAGGACC
A005F39	182 GC	- C		;	CCACAGATATTTGCGGTATGTCATGAGGACTGGGGATGTCTTCTATTGGCCJGGATGTCTTCTATTT
			AGTAAGGTTA		GCTGAGTTTTGTATCTTAGTAAGGTTACTGCACCTTACAGAGIAGICTCAATTTCCCCTGATTTAGGA
mgp.			GCACCTTAC	CCTAAATCAGG	CTROPOSCITACI COTAMATCAGG AGGCGATGCTAATGGGTATTGCATAGGTGTAAGTATAAAAATGTTGTATTTAAGAAATGCCACAAG
A005F42a		42 A G AGAG	AG	GGAAATTGAG	CTTGGTATAAGGCAGAAAATAAATGGTATAAGGCAGAAAATAAAT
1000		-			ATGACAATGATGATAGTATTAGCCTACCGTTTGCTAAGCACCTACTGCGTATCAGGCACCTGACTCGG
TIGH		ි -	CCTGACTOG	COCTGGCTGTG	CACCTGACTOG COCTGGCTGTG TGCTTTACIAGITACATTACCTCACAGGGTTGGCAAATGGTCATTTTGACAAATGGTCATTTIG
A005E46		A G GT	76 A G GTGCTTTAC	AGGTAATGT	ACAC
		-			
		<u>8</u>	GCAGGGGTGA		AGAGCAGGGGTGACGTATGTAGAA(CTJGCTTAGGGTGTCCTCCCCACAGAGCAGCAGATACTTGAACCG
		<u>ರ</u> —	STATGTAGA	GGGGAGGACAC	CGTATGTAGA GGGGAGGACACACACTCCTATTCTAAAGAGCACHHIGHULIGHULAGAAATTCCCCAAAGAGCACTATGCCCC
U20979	24	24 CTA		CCTAAGC	AIAGGAIGCIGGAIIAGIICCIIIGAIAIIIGGAAGGAAG

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		AGTGGAACCA ACGATCATAT	CATTGACAGAA TAAAATGAGGC	AGTGGAACCA CATTGACAGAA AAAAATTAGACAAGTCTAGTGGAACCAACGATCATATCTGACJTATGCCTCATTTTATTCTGTCAAT ACGATCATAT TAAAATGAGGG GAAAAGCGGGGGTTCAATGCTACAAAATGTGTGCTTGGAAATGTTCTGACAGCATTTCAGCTGTGAG
X57830 1	106 GC CT	<u>ਂ</u>	¥	<u> </u>
				AACCTGAAGAAGTTACTGGGAGCTGCTATTTTATATTATGACTGCTTTTTAAGAAATTTTTGTTTATG
_		CTTTTTAAGAA	GGGCTTAAAAA	CTTTTAAGAA GGGCTTAAAAA GATC[T/GJGATAAAATCTAGATCTCTAATATTTTTAAGCCCAAGCCCCTTGGACACTGCAGCTCTTTT
	_	ATTITIGITIA	TATTAGAGATC	ATTTTGTTTA TATTAGAGATC CAGTTTTTGCTTATACACAATTCATTCTTTGCAGCTAATTAAGCCGAAGAAGACGGGAATCAAGTT
X74070b	72'T	72'T G TGGATC	TAGATTT	GAA
				ACTGCCGAAGTGTAGCGGCCCCCAAACCTTGCTCTCATCACCAGIC/IJTAGAGCTTCTTCCCGAAGGG
				CCTTTAGGATAGGAGAAAGGGTTCATGCACACACGTGTGAGAATGGAAGAGCCCCCTOCAGACCACT
				CTACAGCTGCTCTAGCTTGCCACTAGGAAGTTTTCTGAGGCTGGCT
248804	44 CT	L		TCCA
: I				ATGACCAAAGCCACCACATTTAGAACTTTGGCTGOCTTTGGAAGTCCAGAGCTGGATCTCTCAGCTCC
				CGCCCCAGAGGGTCAGCACTTTGGACATGGCTCACAAGCAGTTTTTGATTGA
				GJTGTGCGTGCAAGCATGAACCTTGTTTAAATCAAGAGGCTTACATAATTTTAACCAGTTCTGTCTTC
D28513b	133 A G	 <u>ত</u>		AGCTGTACATA
				OCACTCCATGCTGATGCCCCAAGTTATCCACAGCCTCCTTOCCGACCAAGACCCTATCCACCTGGACC
				TOCATTTTTCCCTGTAA[A/G]TTCTCCAACTGATCCTACCCTCCCTACTCCTGCACCCCAAATATGAA
D29833b	85 A G		•	CAACTGCAGCAGGTGCCACCACCACACAAAAGACACCACTACCCTTGTAACTACTGCTTGTAC
				CCACTCCATCCTGATGCCCCA[A/G]GTTATCCACAGCCTCCTTCCCGACCAAGACCCTATCCACCTGG
				ACCTCCATITITOCCTGTAAATTCTCCAACTGATOCTACCTCCCTACTCCTGCACOCCAAATATGAA
D29833a	21 A G	<u>:</u> ජ		CAACTGCAGCAGGTGCCACCACCACACAAAAGACACCACTACCCTTGTAACTACTGCTTCTGCTAC
	!			CTCCCTGCCTCCTTCCTGCCTGTGATGCTCCGTCTCAAACAGCCGAAACCTGTCTTGCAATGGGGG
				GAGGGGGGTTTC[G/A]CTTTCCTTCTTGGCTTCCTCTTATTCTTCCACAAACCATTCTCAATAAA
				GCCAAAAATCTTTCTTCTCCCCTCAGGCCACCTCCTGTCCTCACTCCTGTCCTGTGCTGCTGCTGCTGTTTT
D31762	82 GA	Α	•	CTGGA
				ATTATCGCGAGTGGTTGACCTTACACTTACTCCTTAAATAGCAGTGAGTAATGCATTTGAGCTG[1/C]
				CCCAGGCTCTGTCTCCTCAGCTCATTTCCTACTCTTTTCTCTATAACTCATTCTATTAAATACATT
	-			GCACCAAAGAGATATGGAGACATAAACCTGTAATGAATGA
D37931	64 T C	<u>.</u>	:	Ш

		CAGGCAGGACTICAGIGICAGIATCCCTGCCTTCAGICTTCTTTAGAAATCACATCGTGTTCAATCCAATACACAATGATCACAATTAGAATCACAATTAGAATGAACAATAGAATGAACAAATAGAATGAACAAATAAAAAAAA
D63807 101 CT		AATGCAGAGGAGTCTGTTCCTCCCCGTCGGCTTCTCGGTGCTGCGAGGGGTGAGCGTGCCCCCCCC
	·	TGGGAACATGCGTGTGACCTCTT/CJACAGCTACCTCTTCTATGGACTGGTTATTGCCAAACAGCCACA CTGTGGGACTCTTCTTAACTTTAATTTTATTTATTTATTT
		TTCACAGTGTGTTTGTGATTGTTTGCTCTGAGAGTTCCCCTGTCCCCTCCACCTTCCCTCACAGTGTG
D90145 21 T C		TCTGGTG
35		ATTATCACTCTCAAAAATTTTGGTGTGTGTTTTAAGTACTTTCTTATTTAT
1a 59 T C		CCAGACATGTTATTATCAAGCCCCTTATATACCATCTAAT
FST16668		GCATTTTAAAATTCACATTGAATCATTATTACTATTTATGATGTTTACATAACAATTCAGTATCATT
5 71CT		ATGIC/TITGTAGATTTCAGATGTAGGTCGTCAATACTGAGCACTTATCT
FST16904		ACAGACTATCGCCAACTTATAATGCTTAAACTTTATGATCAATAGTAATAAATTACAC/IJGAGAIA
SZICT	;	TTCACACTTTATTATAAAATAGGGTTTGTGTAAGATGATTTTTCCCAACTGTAGGTTAACAT
rectores 2	! !	TTTTAAGTACCAGAGGCACTGCTGGAACAGGATGAAAACTGATACACC(AGGTTACTACTTACTC
49 A G	;	TTCACTCTTCAAACTGATTCCCCTAAAGACTTCTACTTAGCAAA
CCT21885	:	GGCTGTAAGTAGAATCAAAGGTTAAGAACATTTTATGCACTTATTCCACAAACATTTACTGAGCATA
E 312 1003.		CTAGGTGCTGGGAIG/AITGTGACAGTGAGCAAAAACACAAA
EC122623		ATTTTAGTGCAAATGACAAAGCCCAA(AGJAGAACAGAGGATCAAATAAGATTGAAATGTATTACC
	;	TTCTCATAAGTATACGAAGTTTAACACAAGTATGGGAGT
00a		AAAATGATTGAATTCAGCAAGTACATTTATGATCTATCTA
	:	AAATTTTTAAAATGATTATCCATTATTTACAGJAGJAAATGTGGAAAAGATGGCTTTTAAACCC
200000000000000000000000000000000000000		CCTCATTTATTTAAAAAGACGGACATAAAAA(T/AJTATACAACAAAAAAACCCAAGTCACATTTCAG
311 A		GAGGTAAAAACTAAAAAGTCTGATATGAAAATATGGTGG
		AAAGATCTGGCATTATTCACATCATCTAAATATTTTGTAATTACTTTTTCCATGAGTATTTTTCA
EST24246		TGTCCAAGCATTTTAACTATCATTTTAGCGTAAATACC(T/C)GAATAACCCATAGTTACAGAATTGG
7 106 T C	.:	GICTGTGTAACCTCAATT
EST24308		TAGTITAATITICTGAACCTTTGGCTTATAAATTTTTCTCAACTT[AG]CATTTAAAAATGTATCAAT
3 45 A G	;	GCACCTICTICAGIAGIACCACATGAAAATATAAACCTCGTIC
ECTOMASE		CTTGAACTTCTGGTCTCAAGTGGTACGTCCCTCCAACCTCCCAAAATGATGCGATTACAGGCATAAG
73 GA		CAGCCIGAJTGCCTGACCCACATTTCTTTATCCGATCTGTTGATGGACATICAGGITGTTC
ST25089		TATTGTTGCATTATCAAAATGGTTAT/CJAGTTTTCAATTAAAACTGTAATTGATTTCTATGTAAA
6 25 T C	_:	ACAGCTTTGAAGTTGTAATGTAGTTTCCAATCGTTAGTTA
		-

EST25476			AATGATCTTTATTTCAGACCTGCTCCTAAAA(GA)CTTTCTCCTCCTAAAAAAACACAAACACA
6	33 GA		AGAGGTCCTCTTGCTTCCATGGACTGTGGCGGCTGTGGACTTGGACUGTCTGCTGA
FST26183			AGATAATGCATTAGAGCCTGCCTCATTGTATCTTGATTAACTTTGTAAAGATTGATCTCTAAATAAG
	70 T A	:	ATIT/AJACATTCTGGGGTACTGGGAGTTAGAACAAC
EST27231			AGAAAATAAGGTGCTACCAGAACTCATGTI/C GATAGCGCTTTCTTTAGGCACATATTATAGCATT
Ta E	28 T C		CAGATGAAAGTTCTGTAATCACACACACTGTGCCTCTAACAACAAAAAAAA
T27816			CAACTCAAGGTACAAGACAATTGCAT[T/CJTAACATTGTTATAAATAAAAGGAACATCAGATCAAT
	26 T C	:	CATTAAGGGCTCCAGAGTGAACAGCATCTTCATAACTTCCATGTT
-			GTTTAATTGGCGTATGGTTCCACAGGCTGTACAGAAAGCATGATGGCTTCTGGGGAGGTCTCAGGAA
FST28588			ACTTACAATCAJATJGGTAGAAGGCAAAAGAGAGGAGCAGCATCTCTTCCATGACCACAGCAGGAGG
	78 A T	;	AACAGACAGAGGGGGAT
			TACTCACACCGACATACATATCTCA(A/C)GTAGAATTAGCTATACTGCATACTAACTTCATTGTAGT
FST30226.			AGGGAATATAAACTACTGAACAAGACAGACTTGTCTAACTTAAACAAGACAGAC
	2 T A C	;	9
,	2		AGCTATGGTAGAGCAAATTCCAGTGGTGGTAAATCAAGAACTCTAAAGTTCAGTAGAGAGGGGT
CCT30036			GTTTGAATGTCAAGGAAATCACTGAGGTAGATTTGGGATTACAATAAGACAGCTGOCCTGTGAGGT
		:	CATAAGAGCTTTTGTGAGG
)		CCGAATATAAGGAAAAAATGGTGGCGG/AJTGCCTCTAAAAACCTGTTGAATAGAATAATGGCCAAAT
ECT30515	-		ATTACAGITTICTCACTITICCTATGAATACTGGCACTGTTTATTTCATGTTATATGTGAGTTTCTATGC
7	25 64	:	ATAAAAATCCCAGTAAGA
			TGCTTTGTTTCCCTCCAAATCCTAAAQT/CJGTGTGTCTTCAAAGAAATTCGTGGAAAGGACTTTGAA
EST33274			TACGAGITTGTACCATATTCAAGTATTCTTGAATACAGGTTTCAGATAACTATGGAGATGATACCATT
	27 T C	:	GGACTAGGTA
FST3352			TACACATTATTCAAGAGCCACCTGACATGCATCTCCTCCGCAGAATACATTCGTCCTCTTAGAGA
7.00	75.0.6	;	AGTTTAA(C/G)GCACATAGTATTATTTACTAAGAGAATATCTCTTGGTGTCATATCTAGGGG
			ATTITICCCACAGCAGAAGTATATTTATTGTGCTGAAATCAGGTAGCAGGGAATGAAT
LETOSASA			GAACCAGTACAGAATGTTCACAAAGATTTACAAATCTCAGTCATTACACACTGAGCAACJACJAAA
	126 A C	;	САААВВТЕСТЕТ
			CCTTTGGGGGGAGTTTTAAGCCAGAATGTGACAAAGTCACTTACAGGAAGACTGGAATGTAGCCATAG
EST33488			TTGAACTCTAACATCGTCTATAGA/GACCATTTCCCGTCTCCAGTTAGGIICIAGGCAIACIAAAC
	90 A G	;	2000
EST33508	: -		AAAAACATGCTATTTGAACAAACTTTTTTATAAAGAATAAGTTGA(CT)TGAAAAGCAGIIIIAAAI
10	45 c T		AACATCAACTCACAAATGACTTTTAGAAGCCAAATAA

EST33508	- 0		AAAAACATGGTATTTGAACAAACTTTTTTATAAAGA[A/G]TAAGTTGACTGAAAAGCAGTTTTAAA] AACATGAAGTGACAAATGACTTTTAGAAGCCAAATAA
Ceranea	5 V 05		ACAACATAGGACTGGTTATTCTTGGTTTTTGAAAATTATGTTGCCACTTCCTATTGTTTAAAAATGA
4	77 C T	;	TCATTTAACIC/TITGTTTGAACTACAGCCTGAATCCCCC
			GAAGTATCCTTCCCAGTGGCAGGAACTGAAGACTCCAGATCAACCAGGTGGACCTTTTCGTTGATGA
EST34739			GCTGATAGCTTCTAGGCTGTGGGGAACCTC[T/A GGTGCCTTACAACTCCAACTACTGCAGAATTTCT
	97 T A		TGTTGTGCCTCATAAACA
		-	ACCTGACTGCTTTAAAAGCTCTTTGTAAGCTGACCGTAGCACAGATCACGTGGCATCCACTATCAATA
EST34792			CTCATAAGTCTAATTTATCCTCAGGATGTTCCCTGA[A/G]GTATTCAGGAATTCTTAGTCTOTAGTACA
. P	104 A G	1	AAGATTTGTTGCTGTG
EST34835			GGAAAATGTTCCCTTTGCAAACAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGAIIICIG
q6	93 T G	:	TGGGGAGTCTATGTTGTGCTTTCTGGTT/GGGCCTTAAAAGAAACAGACAAAIIIGIGCTAAAAGAAACAGACAAAIIIGIGCCTTAAAAGAAACAGACAAAAIIIGIGCCTTAAAAGAAACAGACAAAAIIIGIGCCTTAAAAGAAACAGACAAAAIIIGIGCCTTAAAAGAAACAGACAAAAIIIGIGCCTTAAAAGAAACAGACAAAAIIIGIGCCTTAAAAGAAACAGACAAAAIIIGIGCCTTAAAAGAAACAGACAAAAIIIGIGCCTTAAAAGAAACAGACAAAAIIIGIGCCTTAAAAGAAACAGACAAAAIIIGIGCCTTAAAAAGAAAAAAAAAA
FST34835			GGAAAATGTTCCCTTTGCAAACAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGAIIICIG
- Ba	82.GA		TGGGGAGTCTATGTTIGAJTGCTTTCTGGTGGCCTTAAAAGAAACAGACAAATTGGGGCTTAAAAGAAACAGACAAATTGGGGCTTAAAAAGAAACAGACAAATTGGGGCTTAAAAAGAAACAGACAAATTGGGGCTTAAAAAGAAAAAAAA
CCTCTCT			CACAAAGGTCCACTTTACTTACATGAAGGAACATAAAGGCATGAGAAACAGTCATCTCAATAAATG
0	93 GT	-	CAAGACATGAGCATAAAAGAGGTTCTGGTJGCCTTTCCAGCGTTGTTATTACAGAGAAACCT
			TOPICALOTACOTACACTOSTICA
EST35337			TCTTTTCAAATTTTTGATGTAGGCATTTAATGCTTTTTTCAAATTTTCAATTTTCAATTTTTCAATTTTCAATTTTTCAATTTTTT
6	33 CT		ATATCTCAGAAGTTTGGGCATGTTGTGTTTCCATTTTACTTAGTTCAGAACTTTCCAATTTCAGT
			CTGCCCCAAATTAACTTTTAGGCAAATGGAAA(C/T)AGACTTACTGTATGGGGACATTTTTAAAAAG
FST35708		_	ACAGCTTAGTAATATGTTCATATGCAGCGTGTTGCTTCCCTCTCTGAGGTTGGCACCTTTCTGTAGGTTGGCACCTTTCTGAGGTTGGCAGCTTTGTTGTTGTTGTTGTTGTTGCTTGC
0	32 CT	. :	ATGTGCAAAGTGTGGCT
			ATCCAGTGCAGAGTTGTAGCTGGAGACATATTTCAACCCACAAAGGCTCCA(C/G/ATGTTAAAACGT
EST35747			TTCCCAACATCAACCTAATACAGTGACAGCAACAOCTCCCTCCTGCCCTTCCAGTAGGGTIGAGATI
	5106	-	9
,			TGGTCCATTATATATAAAACTGAGGAACAAACGGTGCTGACATGGCAGACATTTATTT
ECT35751			AGTTCCTCCCATGAAACCAAGA(CA)CTTGTCCTCATGATAAAGTGGAGACAA I AAGAAAAGCCAAGA
5	89 CA:	-	ATATAATTAAGGCCTGTGA
,			CACCTGTTCATTGGTTCACTGGGCTGCTATCTGTGGGCTGATGCTCTACCAAGTGCTCAGGCTACAGC
FST36301			AGTCAGGAGGCAGCCATGGCCCCTGCTJGCTGATGGAGCTTGTAATTAGCCCCAAACTGATCTTCA
4	93 CT	:	GAAAGAGGTACAACAAA
	:		GCCATCAGCCCACAAAGACATGACTACCAACGCJG/TJGGCCCCTTGCACCCATACTGGCCTCAGCAC
EST36519			CTAAGACTGGACAACTTTGTACCTAATGACGGCCCCCCCGGCAIAIACIGGCIGGCIGGCIGIGCIGGCIG
0a	33 GT	:	CACAGGGGTCTTAGTCGT

EST36620	SO G		GACTITATTAGATAAGGGGTTTCGGCTACCCTCAAAGCTCTCAGGAACTGG(GAJGCTAGGGTTTAAGGAAAGGGCCACACCCGATGCAAAGAATAAAATACAAAAGGGCCACACCCGATGCAAAAGAACTTT
			OCTGTGATGTGCATGGGTGCCTGAGCAGTCGTACTTACTATGCGTCAGACAGCTCACGTATGTCAGGA
EST36690			AAGGAAGTCTGGGGATTCCTA C/GJAGGGGACATATCACACATATTCTAAGTCACTGTGTGACTCGG
0a	89,CG	•••	СТТВАВСАЯВТСАТТТСА
EST36729			GAGACAGAAGCCATCAGTTAAATGAGGTTAGGCCTCTCCTCCTAATATACTGATTGACAATG(C/T)A
6	62 CT		TATTAGCCAGGTAATGCACTTTAGCTACCTGGACAATGCTATCAAGTGTGCTGGGAAGGGAAG
		٠,	ACTGTCTGGCCGATGATTGGAGCTTGAAAAAACTACCATGCCAGATCTCCACCCCAGACCAATTAG
EST36823			GTCAGTATCTCTGGGGGTGCTATTCAAGCAACAATT[A7]TCTTTTATGTTCCTAAGCTCATCATGAG
9	103 A T		TTAA
			ATGATCGCTTATGTAATTTGAGGGCGACATGGGTAATGGGAGATACCCCACAGGACCTGTAAATATT
EST36987			TAAATAATATTTAACAGCTGATCAGAGGCTAAATTACAACTGACATTTTGATGCAGTTT[C/G]GTTA
4	126 C G	:	GGGAATTAAGACAATGCAG
			GGTCTCACTCTTGCCCAGGACGGTTTGAAACTCCTGAGCTCAAGTGACCCTCCCACCTTGGCTTCC
EST37054			GAAAGTGCTAGGATTACAGG[T/C]GTGAGCCACCACCACGTGGTCCTTGGTTTAAAGTAACCACTGAA
8	88 T C	:	O
EST37269			AATAGTCTATGGCTACGGGCCCGTGGGATGTTAAAAATTGGGATTTTAAATTAAGATTGTGAACATG
3p	105 T G	:	CAAACCCAGCAAATTTCTCAGCTTATATTTTGAAAGTCTT/GCAGGAGAAAAAATGGGGGTCC
			AAAAGACCTTTCTCAAGCAGTAAACTTTGAGCAGAGACTCAGATGAAGTAAGGGATGAACCAGGAA
EST37284			GCTCTCTGGATAATGTCACTCTAGGAAJG/TJAGTAAACAGGTGTTAAAACCCCTGAGATAGCAACCCT
2	93 GT	:	CTTGGCTTGCTTGAGGAATA
			AGATGGGGTCTTGCTAGCTTGCTCGGGCTGAACTAAAGATATCCTCCTGCCTCAGCCTCCCAGGTAGT
EST37315			TGGAACTATAGTAGGAGTATCT[A/G]CCCTGCCCTGCTAGAACTTCAAGTTTTGATGGGCAAATOCA
2a	90 A G	1	CCCCAGAGGACAGGACAA
			CCTGCCATGATAATGTTAAAACATATCAAGATCCTCCTCAAACTT[C/T]AAGGGTGAAAAGCATACC
EST37374			ATTCCATTTTAGTTGAAATATTCCTTCACATAGCCAACACATTTTTCAAGGCACTCTAGCTACTACA
-	45 CT		V99)
			GTGACATCATGTCTCTTCAATGCCCTTTCAATTAATAGTAGTTGAGCGCTGGGGGCTGAAGTCAGACT
EST37376			CTCTGGGTTCAAATCACAGTGCTGTGTCCTGCAQQCJGCTGTCCTCAGGCAAGTTGCTGACTTCTCTG
8 b	101 GC		TGTCCAGG
			GTGACATCATGTCTCTTCAATGCCCTTTCAATTAATAGTAGTI/CJTGAGCGCTGGGGGGCTGAAGTCAG
EST37376			ACTOTOTGGGTTCAAATCACAGTGCTGTGTOCTGCAGGCTGTOCTCAGGCAAGTTGCTGACTTCTCTGT
Ba	41.TC		GTCCAGG

FST37378			ACACACAAAAAAATGGTGGCAGAAAATCTGGAAAGATTCTAATAACCTCAATTCGTGAAAAG 1/G
	63 7 6	;	MACATGCCTCAAAAAAGAGGGGGAAAAACTTTAACAGAAACACTGTGCTGACATGATTAGCTT
ECT37452			AAGACATAAATCTGCAATGAAATCAGTTATGAAATATTAAACCTCT[G/A]CTTCTCAGGAGTGACAC
	46 GA	_:	TAATCATGGTCTGGAAGCTAGCCTATCGCATTTTAAAACACCCTTAAATCAATGACGTAGAA
			CTAGGCATGGGGCTTTTACAGTCATTTATTACQAAGGTCATGAATTCATTAAAAACCACAGCGAT
2012/013	7	_;	ATAGCAATGAGCAAAACAGACCCTCCCCCAAAATCACCCTGCGTTCATGGATCTTCCATTCTAA
ECTSBOSE	5:		TTATTGAGTAGCTACACTGTGGCCAGAACTAAGCTTTACATGTTTTATATCACTTATAGTTATCTCA
	76 ⊤	:	ACAATCTTGAAAGGGTGGTATTATTTCCCCGTCTTATAGGTGAAGACTCTGAGGTTCAGAA
EcTables			TCTACCAGGTCACCAAAGTATCTGTATATGCTTTAAGTGGCATTTTCATGTCACTTACTCGCATGG
	٠٠ ا ا ا ا ا ا ا		AAGAACGCTCTCCTTTTAATTCCCTAACTCTTCTTCTGGGAAGACAGAACGTGCACAA
			TABATCAAGGCCTCTTTCATTACCAAAACAAAAAAAAAAA
- 00100			GAAGAGATGCCGAAGTGTCATCCTGACTTCJGTCCCTGCAGTGCCCATGGGTCCCGTGCCT
E3138420	1001		ТАТТСАТТСТСТСТСТСА
:	-		THE ATTRICA AN A GET A GEORGE CONTINUE OF THE GEORGE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE OF THE CONTINUE
			CTEGA A TACTTGGGACTTGCATTTGACACAGGGTAAAAGTATGGGATGAGAGGAACAAAAGCTT
EST38950	- (ACAAACAAAAAAAACAAAAAAAAAAAAAAAAAAAAAAA
2	25 C	:-	ACCONCINENTALITY
EST39053	•		TITITIGITACICIGIAGOCAGICALIZANCIA ACATACTORATATITICACCICGIGGAGITG
9	90 T C	:::	TAG ICT HACACAAA I GC I ATG I I CANACAA I I ACT I I ACT I I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I ACT I
			TCCTTCTTGCTCTCTAGCACTCAGACCACCAAAGAAAGCCTGGAAGGCAGCCATGGAAGGAA
FST39331			TGC[GIC]GTGTTTTAGGGAGAGCTGGCACCTGGCCTCTAATCTTCCCTCTGCCATTGACCAGATGGGT
	70 GC		GOCTTTGGATACATCACT
COTABEAA	5		GTCACCATTGACCTTACATAGTGCCTCTAGT[C/A]ACCTATGAGGCACTAGAACTCTATTGTACTTCT
-	21.0		CACTITATCACATTAGCIATCGAAGITIGAAAITI
-			TTCTAATAGCATGCCCTGTGACAGGGAAACTAAGCTC[T/C]TCAAAATAACTGAAACTAAATCTGTA
ECTADEAB			AGATAAAATGCTGGAATTTGAGAAGGCACATGCCTTTTGTAGTTTTCTCCAGAAGGCTCAAGGGTGTTC
10240	37 T C	_;	AATAATCTGTGGGACTCA
			TGTTTCTCTAGAGACCCTGTGTGATACACTACGCATGCACA(A/G)ATAAAGTCACATCAAGACTAA
CCTADEAD	-		TAATCTAAATGTTAGTTTGTTACCACCATTTCTCACTTTGAACCTAGCTCCCTGCAAAGCACCTTCTA
1	40.4	_:	CCCTGCACTTTTGGGGAG
07.405.70	-	!	TGTGAATTACACATCAGTAAGGCAGTTTACAGAATTTTCATTCTCTTACCTAAAGTCTGTGCTATCTG
E21403/3	81:4		AGCTGGTGGAAAAWCJGGACTTGGAGACAGCGATTTAAATACGGAACAAGGTCTTCCAGGAAG
CCTANGOA			TIGIATGGTTGTAGGAATTTGGGAAGAATTATCTGTGAAGGAAATTTGCCACTGTAATGCACACCC
ES 140364	- B		A/A/GITCTGTACTCCCACAATATCCTATGTTTTAAGCT
2	5		

			GATCAAACTGTATTGCCCAGGCCCAGCTCCTGAAGAACTGTGAACTATGAACTAAGAGCCTCTCTAAGCA
FST51340	51GA		Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda Adda
	1	1	CATGGGAGTAATAAGAGCAGCAGCAGCATCTCTGAACATTTCTCTGGATTTGCAACCCCATCAT
			TCTICAGACCITICACAGACAGACAGACACAGACAGACATCAGACCACAGAGACACCAGAGACACAGAGACACAGAGACAGAGACAGAGAAAAGACACATCATCAGACAGA
J04162	134 T C		AGCTG
Γ			CTGAACTCCAGCTGCCCTACAAACTCCATCTCAGCTTTTCTTCTCACTTCATGTGAAAACTACTTCJC
			CAGTGGCTGACTGAATTGCTGACCCTTCAAGCTCTGTCCTTATCCATTACCTCAAAGCAGTCATTCCT
	-		TAGTAAAGTTTCCAACAAATAGAAATTAATGACACTTTGGTAGCACTAATATGGAGATTATCCTTTC
K01506	63 T C		ATTGAGCCTTTTATCCT
			TGAGTCTGAGCACGAGTTGCAGCCAGGGCCAGTGGGAGGGA
			CTI/CJATCCATTAGTTTCCACTGCCTCGTGTGACATGAGGCCCATTCTTCACTCTTTGAAGAGAGCAG
			TCAGTATTGTTAGTAGTGAGTTTCTGTTCTATTGGATGACTTTGAGATTTATCT11G111CC1G11GGA
L18877	69 T C	:	ATTGTTCAAATGTT
			GCTATTTTACATATCCCAAGCCCTTTAGGGCTACAGTTCJCTCTTGTCCTGGACCCTGTAGGGTGCCA
			TTTGGAGTTCACAGCCTAGAAGAAAAAGGCTTTGGGCCTGGTGTGGCATAGGCCTGTAALCGT
			AGCGCTTTGAGAGGCTGAGGCAGGAAGATAGCTTGAGCTCAGGAAGTTCGAGACAAACCTGGGCAAT
L31848	36TC		GT
			GGGTCCAGAAGCCTCTCAGCCAGGAAGGGAAGCTGGCCCTGGAAGGGACCTGAGCTGGGGGACACTGGC
			TCCTGCCATCTCCTCTGCCATGAAGATACACCATTGAGACTTGACTGGGGCAACACCAGCGTCCCCCAC
			COGOCOCATOCATGATCATAGAGCTGCAAGCTGAGCTGGCGAGGGGGATGGTTGTTGACCCCTCT
L38517	137 GC		CTCCTAGAGACCTTGAG
			ACTTGAGAAGCAGAGCTCGCCACCTTCTGGAGGCCACTGTGATGATGAGCAAGCA
			AGTTGAAGGGACAGGGCAACAAATACAGTAGTAGTTTCTTTTGTATTTGTATTT/GJCGCCTGA
			AGATCATCCCGCAAGGCAGGCTGGAGGTGCCGGGCCTGTGTTGCTGGGATTTTAGTCTGTGCTGG
L39059	123 T G		GAG
			CAAAGTTGTCTCCTGCCCATGAGCACCACAGTCAGGCCTTGAGGGGAICTTCTAGGGAAGACAACAGC
			CCTGTCTCAAAACTGGGTTGCCAGCTCCAATGTACCAGCAGCTGGAATCTGAAGGCGTGAGTCTGCAT
			CTTAGGGCATCGCTCTTCCTCACACACACACACACACACA
L41268d	L41268d 173 G A	;	AAGGT

			+ (C + 4 + (C + C + 1 + 1 + 1 + 1 + 1 + 1 + 1 + 1 +
			AAGTGAACAGAAAGCAAAGATGGATTGTGTTCCTATAAAAGCACAIAGIIAIGIIIACIGUAAICUI
			AAGAAGCTGGAAGAAGAGCTCAAGTTTTGGTTTACTTTCAGAATTCJGAAGAACT IATTCAGAAAG
			CAGAAATAATCAATGAGCGATTTTTAGCCCAATGCTCCAAAAACTCATCCTGTACCTTGGAGATCCA
L48728b	1111 T C	:	CIC
	-		GCGCACAGTCCAAAATACAATTGGACAGAAGATCTATATATA
	-		CCATCAAGIAIAAGGI IACIGAIIGAIIGAIICCIIIIAIAAACAIIGAIAGIAIAIGAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICCAIICAIICAIICAIICAIICAIICAIICAIICAIICAIICAIICAIICAIICAIICAIICAIICAIICAIICAIICAIICAIICAIICAIICAIICAIICAIICAIICAIICAIICAIICAIICAIICAIICAIICAIICAIICAIICAIICAI
M18079	52 G.A	:	AGCAAAAGAAGTAAAAGCTAA
			TAGGGATCTGTGCCAGGCCATTCGCACCAGCCACCACCCAC
			TGGACTGGTGGCCCCACCCTGCGGGAGGCCTCCCCATGTGCCTGTTCJGCCAAGAGACAGAGAGAG
			AAGGCTGCAGGAGTCCTTTGTTGCTCAGCAGGGCGCTCCGCCTCCCTC
M19169	113 T C	:	\mathfrak{D}
			TCACCTOGTTCCACAGCTCCACCTGCATCTTCTCAAAAGCCATCCAGGGATACACAGGGAGCTTCT
			TICCCTTAGCCTGTGATCTGCCCATGATCCCCGACAGCAAAA[1/G]GTTTCCTTTCTGAGGCTG
			CCATGCTGCCACTGTCCAGGTGGAGACTGAGCAAAGGAAGTCCTCAGCTGTACCGGCCTTTCAGAGCT
M21539	114 T G	:	TCTCTTTGGGTGC
			CCTAGCATTATTTTCTGGCCCCATTTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCTCACCTCT
		-	TCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAAATGCCTTTGAATTATTTCCCTGACTTC
			CTGATTITITICITITICICCAGTGTTACCTACTAAGIAGIGATGCCTGGAGTAAGCCACCCAGCTACC
M26041c	173 A G	1	TAATTCCTCAGTAA
			CCTAGCATTATTTCTGGCCCCATTTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCTCACCTCT
			TCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAAATGCCTTTGAATTATTTCCCTGACTTC
			CTGATITITITICITITICTCA[A/G]GTGTTACCTACTAAGAGATGCCTGGAGTAAGCCACCCAGCTACC
M26041b	M26041b 157 A G	•	TAATTCCTCAGTAA
			OCTAGCATTATTTCTGGCCCCATTTATCATATCCCTTTTCTCCTCCGCAAATGTTTCTCCTCTCACC
_			TCTTCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAAATGCCTTTGAATTACTGCGTGAA
			TTCCTGATTTTTTTCTTTTCTCAAGTGTTACCTACTAAGAGATGCCTGGAGTAAGCCACCCAGCTACC
M26041a	45 C.G	:	TAATTCCTCAGTAA
			TAAGGCAGCTGTCAGGGAGGCCCAGTCACAGTCCAGCATTCCACAACCACCTTGAQGCCAATGCT
		·	TGCCAAGCTGTTTTAAAGCCAAGAACACCCTTTCTTTGTTCCAAATTAACTCTTAGAAGAAACCCCA
M63967	57 GC	1	CAAATAAAGCAATTCAATC
	!-		ACTTACTTACCCTCACCTGTCAGGCTGACGGGGAJGAJGAACCACTGCACCACCGAGAGAGAGGCTGGG
			ATGGGCCTGCTTCCTGTCTTTGGGAGAAAQGTCTTGCTTGGGAAGGGGGCCTTTGTCTTGTC
			CAACTGGAAACCCTTAGGACAGGGTCCCTGCTGTGTTCCCCAAAAGGACTIGACTI
M81695	34 G.A	***	

				CTCCTCCTITATTTCAGCATGGGGGTTTAAATGGAGGATCTCCTTTTCCTGTGACAAAACATCTTTC
				TATTITICCAGGCIATITAATACGIACTITIAG(C/I)TGGAATTATTCTATGTCAATGATTTTAAGCIA
U06641d	166 CT			
				TGGCCTGTAGAATAGCCTGTGGCCTTTGCAATTTGTTAAGGTTCAAGACAGATGGGCATATGTGTCAG
				TGGGGCTCTCTGAGTCCTGGCCCAAAGAAGCAAGGAACCAAATTTAAGACTCTCGCATCTTCCCAAC
100960V	39 TC	···		сстта
				GAGCAGAAGGCAAGAGGCGCCAAGATGAGTTTTGAGCGTTGTATTCCAAAGGCCTCATCTGGAGCCTC
				GGGAAAGTCTGGTCGTTCJACATCTGCCCGCCCTTCCAGCCCTTCCCCAGCCCCTCCTCTTGTTTCTTC
009608	82 T C	: 0	:	ATTCATTCAACAAATTTGGC
				GTGACATGAGGCCCATTCTT[C/G]GCTCTGTGTTTGAAGAGAGCAATCAGTGTTCTCAGTGGCAGTGG
				GTGGAAGTGAGCACACTGTATGTCATCTCTGGGTTCCTTGTCTATTGGGTGATTTGGAGATTTATCCTT
	-			GCTCCCTTTTGGAATTGTTCAAATGTTCTTTTAATGGTCAGTTTAATGAACTTCACCATCGAAGTTAA
U10694	20 C G	···		TGAATGACAGTA
				AAAAAGGACTCTGGTTCAAATCCAGGTTCCATTTTGCTATCTTTGTGACCTTGCACAAGTTGTTAAC
				CICTITGTICAGAAATTICICCATGGAGTAACAATATCTAGGTTGGGAGGATTAGTGAAGTTACATGT
				AAAGCACAGAGGAACAGCCAAGAGAT[T/C]TTACCGTGGTCTTACTAAAGTACATATCCTAACTTGG
U13877b	162 T	:		GGTTTACCTTCAGCA
				TITCTGTCCACTTTCACCTGGTTTTAATAGCCAGCCAGTCATAATAGTAGAGGAATCAGTCAAGCAA
				AAATGCTTTGGAAGAATTAAATAAGCAATGCTGAACATCAGGAATTGTAGATATCCGTACAGAGAGT
				TCCAGTAAAATTTTATGAGTCCACGACCCCTTTTCTAAGCAGTCTGGTCCATG[T/C]TGGTCTCATAC
U15555	187 T C	··· O	•	CTCATATGCAGGATTCATTCA
	-			TOCAATTATTGGTCCCCAAAAGCAGCTTCCAACGTTTGCCATCTGGATGACAAACGGAAGATCCACT
				AAAACGTCCACGGGATTAACAGAACGTCCTTGCAGACTGAGCGATGACACCACACTICITTGG
				ACATTTAAATTCACTCTGCTGAATAGGAGGAAGCTTTTCTTTTTCCTGGGAAAACAACTGTCTTGG
U17077	122 T C	 		ААПТА
				GCACATGCAGAATAGACTCAGCCTATGTCCTGATTCCAGCTGGGTAGTTCTAGAACTITT/CJAGAAG
				CTCCATCTTTTAATGTTTTTATTGTTATGTCCCCCTCCCGGCTTCCCACCTAAATTTAGAGCTTTAAA
				AGATGCACTGCCCAAATAGGACACACGATGGTGTTAGCTGAAGTTTGATTAGCAATTAGGCACTTCC
U18543		58 T C	_:	AAGGCTTTAGTAGAGAGAGCC

			TCACTGCTGTGGCCTCATACTCTTTTTCCAGAGAAGCCTTTTAGTATATGAAAATATTTATT
			AAGACAACCAAGAGAAAATTGCAAAAAGA(CA)AAGTATGACTTTTATATGAACCCCTTCTTTAGG
U25975b	164 CA	<u>:</u>	GTCCAGAAGGAATTGTGGACTGA
			TCACTGCTGTGGCCTCATACTCTTTTTCCATTTTCTACAAGAAGCCTTTTAGTATATGAAAATTATT
			ACTCTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAA
			AAGACAAC[C/G]AAGAAAATTGCAAAAAGACAAGTATGACTTTTATATGAACCCCTTCTTAGG
U25975a	143 C G	:	GTCCAGAAGGAATTGTGGACTGA
			CAGGGAGAGGTTATTCACAACCTCACCAAACTAGTATCATTTTAGGGGTGTTGACACACAC
			TTGAGTGTACTGTGCCTGGTTTGATTTTTTAAAGTAGTTCCTATTTCTATCCCCCTTAAAGAAAAT
			GCATGAAACTAGGCTTCTGTAATCAATATCCCAACATTCTGCAATGGCAGCATTCCCACCAACAAA
U25997	61 A G	;	<u> </u>
			ATTCCTGACAGCTAAATTAGCCCTAAATGIC/TIGGGTAATATTTTCCTCATGTTTTAAAATGAGGTT
_			AATATTTGCATAAAATCCTAAAACAGACTTCTGTATAGTTTATTTA
			CAGATGTTGTGGCCTGGGAAAGCCCTCATTGCTACAGTACAAGTAACACAAGTCGTTGTACCTCAGTT
U28413	29 CT	_:_	9
		-	TAGGGGTAGCATTTAAGATTCAGGAGTCATTAGCAGTGATGATTTTGGGACCTGCCGTATAATCTGTT
			CTTCTATTCCCACGTTAGCCAJA/GJTTGTTCTTGATGAATCTATATGAGTCATAGAACACAAATCTAT
			TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACTTGCCCACAGTTGAACAAGT
U30884c	89'A G	:	GCTGTCA
	-		TAGGGGTAGCATTTAAGATTCAGGAGTCATTAGCĮA/GJGTGATGATTTTGGGACCTGCCGTATAATCT
			GTTCTTCTATTCCCACGTTAGCCAATTGTTCTTGATGAATCTATATGAGTCATAGAACACAAATCTAT
			TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACTTGCCCACAGTTGAACACAGGT
U30884a	34 A G	:	GCTGTCA
			GGGACAGCATATGTGGCACCGCCTCTGTGCACGTGAAGACCAATGAGACGGCCTGCAACCAAC
			GCCGTCATCAAJA/GJCCCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA
			CCAGCACCAAGACCCTTTACAACGTAGAGGAGGAGGATGCCCAGCCGATTCGCTTTAGCCCGCC
U31216b	78 A G	:	TGGTAGCCCTTCCAT
	-		GGGACAGCATATGTGGCACCGCCTCTGTGCACGTGAAGACCAATGAGACGGCCTGCAACCAAC
			GCC[GAJTCATCAAACCCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGGCCTGACCTTTCAGATA
			CCAGCACCAGACCTTTACAACGTAGAGGAGGAGGAGGAGGATGCCAGCCA
U31216a	70'GA		Tracinosi

U31416c	76 G A		<u>;</u>	AGITIGOCAGCICCCATGTACCAGCAGCTGGAAICTGAGGGGTGAGTCTTCATCTTAGGGCATCGCTC CTCCTCACGA/GCACACACAGATCGCTGGTGCTTGCTTACAAATGTCAGGTCCCCACTGCTGCT GGAAAGAAAAACACACACTTGCTTAGCCCACAGTTCTCCATTTCACTTGACCCCTGCCCTCTCC AACCTAACTGGCTTACTTCCT
				AGTT GOCAGC TOCCATG TACCAGCAGCTGGAATCT GAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC
				[C/TITCCTCACGCCACAAATCTGGTGCCTCTCTCTTGCTTACAAATGTCTAGGTCCCCACTGCCTGC
				GAAAGAAAACACACTCCTTTGCTTAGCCCACAGTTCTCCATTTCACTTGACOCCTGCCCACCTCTCCA
U31416b	68 C T		.	ACCTAACTGGCTTACTTCCT
			٠	ACGGGTCACACAGAGAAACCTGAGTCTAGCCATGAGGGGCTTATGCTCCCAACTCACATTGTTCCTCC
				AGACCGCAGGCTTTCCCCCAGCCTCAGGTTGCTGGAGCTGTCACATGACTGCATCCTGCCTG
				GCTGCAAAGCAAGGTCTTGCTTCTATCTGGGGGACGCTGCTCGAGAGAGGGCCGAGAGGCCGCAGAAC
U37519a	78 CT			ATGCCAGGTGTCC
				GACCACGCTGAAACCCACCCACCCGCTGTGCTGACCATGGGCCCTGAGCGTCCT[A/G]CCCGAATTC
				ACGAGGCTGAGGCATCCGGGAGCTGGCGTAATGCCTGGCCGCAGTGTGTGT
U37690	54 A G	i		CTGGAAGGAACCATCCAGTAAAGGTCTTT
				TGAAACCGTTTCAACATGGAAATGATCTGTATTGACTAATTCJACACCAGTCCACACTTCTATGACT
				TCTGCCATTTCAAAGACTCATTCTCCTATAACCACCGCATGAGTTGAATCAAAATTTTCAGATCTTT
				TCAGGAGTGTAAGGAAACATCATGTTTACCTGTGCAGGCACTAGTCCTTTACAGATGACCATGCTGATT
V00540	39 T C			A
				TCAAGAAGGTGACTGCCCTTGTATGATGGAATGGAAGATGAATGA
				AACCACTCTGAGGCTCTCTGAGACCATGTGGTTTTAAAA(AT)ATCCATAAGGGAAGGTACCCACAC
	_			CAGTATCTGAGTTCCAGTAGCTAAGACCCTAGAATTTGGATTCATCTCTGTTTTTCATGTCTCTCCTT
X15943	106 A T		1	GTAACCCTGAGATCATCAG
				AGGAAGATCCCACCGACCCTTCCTGGCCTAATCCTTTAGATTAGGTCACATTACATTAACATTTAGGA
	_			ACCCAGACCGAAAAGTTGCTGAAAGGGAAGGAGACACATTCACAAAGAAAAGTTGCGAAAATTGCG
				AAATCTGTTGTGCA(C/T)GCTCAAATGAAAACGCCTTTCGGCTTTGGGCTTTTATTTTTTGGAACTG
X52011b	148 CT			CGAGTGGCTTAGGTCTAGCCT
				AGGAAGATCCCACCGACCCTTCCTGGCCTAATCCTTTAGATTAGGTCACATTACATTAACATTTAGGA
				ACCCAGACCGAAAAGTTGCTGAAAGGGAAGGAGACACATTCACAAAGAAAJAVCJGTTGCGAAAATT
				GCGAAATCTGTTGTGCACGCTCAAATGAAAACGCCTTTCGGCTTTGGGCTTTTATTTTTTGGAACTG
X52011a	X52011a 118 AC			CGAGTGGCTTAGGTCTAGCCT

				CAGGCCACCTGTCTTCTCCCAQA/SJTGCACAGCTTCCTGAGTCACCCCTCTGTCCAGCCAGCTCCT GCACAAATGGAACTCCCCAGGGCCTCAGGACTGGGGGCTTGCCAGGCTTGTCAAATAGCAAGGCCAG GCACAAATGGAACATTGCTGGAAGGGCTTGCTGCCCTTGTCCCCAGGCCCTGCCCTTGTCCCAAGCCCTGCTCC
X54741	24 A G	:	***	AGCAAGCAGTGC
				AAGCATTTGCGTTTACAGTGCATCAGATACATTTTATATTTCTTAAAATAGAAATATTATGATTGCAT
				AAATCTGAAAATGAATTATGTTATGTTGCTCT[A/GJATACAAAAATTCTAAATCAATTGTGAATTGTAATTGTA
X54869	99 A G			GALGCACACAALIACIAAAGIACAGACAICCIAGCAIIIGIGIGGGGGGGCICAIIIIGCICAAAGIA
	_			GOCGTGTCCTGACACCTCCAGAACGCAGGTGCTGGCGCCCGTTCTGCCTGGGACCCCGGGAACCTCTC
				CTGCCGGAAGCCGGACGGCACGGGATGGGCCCCAACTTCGCCCTGCCCACTTGACTTCACCAAATCCT
X66924	147 GA	::-		TCCTGGAGACTGAJAACCTGGTGCTCAGGAGCGAAGGACTGTGAACTTGTGGCCTGAAGAGCCAGA
				GAAATGTGAAGAATGTGACAAAGCCTTTAAGCGGTTGTCACACTTGATTGTATAAAGATAA[7/G]T
				CATACTGGAGAAAACTCCCAGAAGTGTGACAAATGTGACAAAACATTTAATTAA
	_			TTGCACAGGAAAGCATTTATACTTGAGAAAAATTGTATAAAGAATGGAAAAGTCATTAATATCTGCT
X78932	62 T G	: 5	_;	CATATCTTAACATCAGCGAGTT
				CTCAACCCATAACCTCAACCACATCIT/CITATCCTCCACCCCACATCCCACCACATCCACCTCCATCC
				CCAACCCATCCTCATCCCCAACTACAGCCCCAAACCCAGCCCAGACTAATCCACAGCCATCCCCAA
				CTCATCCTCATCCCCAACTGCAGCCCCAAACCCAACCCA
X80026	25 T C	:		AAACTCAACACCATCC
				ACCICAACTICAAGTCCCAGGCCAGCCATCTTTCCTGCCCTGC
				ceoctegagoaagtectcagctacttctcctjgcjcactttgaaagaccctcccactcctggcctca
X80197b	99 (3	 O		CATTICICITGIGATOCOCCACTICIGGGCTCTGCCACCCCACGGGGAAAGGCCACCCTAGAAAG
	 			ACCCCAACTCCAAGTCCCAAGGCCCCAGGCJA/GJTCTTTCCTGCCCTGCCTTGCTTGGCCCATCCAGTCC
				AGECGCCTGGAGCAAGTGCTCAGCTACTTCTCCTGCACTTTGAAAGACCCCTCCCACTCCTGGCCTCA
X80197a	28 A G	g		CATTICICIGIGIGATCCCCCACTICIGGGCTCTGCCACCCCACAGTGGGGAAAGGCCACCCTAGAAAG
				GGCACCCAGAGTGACCACAAGTCCAGCAGGGAGGGGGGGG
		. —		CAGOCCOGGAGAGGTCCTGADCTGGGGGGCTTCTCCAAGCCTCACTGCGCCADGCTCCCCGGGCTCCT
				CTTTCTCCCAAGGG/AJAAACCAAATGCGCCCCTTCACCTCGCGTGCCCGTGCGAGGCCGGGGGGTT
X85106	150 GA			CTTCAGAGC
				ACCACCAGOCATGGTCTAAGGACATGGATCGGGTGCCCCCAGACGTGTGCACAGGGGACCCTCTGCCC
		-		CACTCTGGGCTTTTCAGATACTCTGACCAAAAAGCCTGCTTTAAACCGCAAGATGGGGGCCTT/G GGGC
				ATGCGCAGGAGGAGCCATCGGGTACTACGCAGCAACACTCACAACTGTCCAGGCTGAGATAAATCCC
X87160	128TG	G	:	IGGGA

				CATCCCAAGGCACTGGTGGTGACTCTGCTTCCTGICTJACTGACCCAGAGCCTCTGCCTGTGCACTGC
				AAGCTGTGTCTACTCAGGCCCCCAAGGGGACTCTCTGTTTCCATTCTCCCCCCACAGAGCTGTCAAGAG
X87344	34 CT	-		AAGCATGACAAAATCATTTACCGACTTTAGTGCTTTTT
		. ——		GGTGGGCTGGTATCTCAGAAAGTGCCTGACACTAACCAAGCTGAGTTTCCTATGGGAACAATTGA
				AGTAAACTITITGITCTGGTCCTITITGGTCGAGGAGTAACAATACAAATGGGTTTTGGGAGTGACCTAGCTTACAAATTAACAAATTAACAAAATTAACAAAATTAACAAAATTAACAAAATTAACAAAATTAACAAAATTAACAAAAATTAACAAAAATTAACAAAAATTAACAAAAATTAACAAAAAA
X87838	179 GT			GTTAAAATT
		:		GTTCTGCTGCCTCTACACAGGGGCCCTGTACAGTGATGGTGCCATTTTCGAAGGAGCAGCAGTGTGA
		_		CCTCCTGTGACCCAAGITGAATGTGCCTCCAAGCGGCCCTGTGTGTTTGACATGTGAAGCTATTGAT
	•			ATGCACCAGGTCTCAAGGTTCTCATTTCTCAGGTGACGTGATTCTAAGGCAGGATTTGAAGGTTTCAAGGTTCTAAGGATTTTCTCAGGTTGACGTTGAAGGATTCTAAGGATTTTCTCAGGTTGACGTTGAAGGATTCTAAGGATTTTCTCAGGTTGAAGGATTCTAAGGCATTGAAGGATTTTCTCAGGTTGAAGGATTCTAAGGCATGAAGGATTGAAGGATTGAAGGATGAAGGATGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAAGAAGAAAGAAAGAAAGAAAGAAAGAAAA
Z14138	B .			SOUTH AND STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF
				TAATCCTCACCATTCCTCAGGTATAAGIICIAIAAACAGGCIIGGAAICIGGGIAAIIAAAAAAAA
_				AAATTATAGTCAATATACCATGACATGAAGAA GAATCCA I CI I I GGAGA GAATATAGA GAATATATAGA GAATATAGA GAATAGA
				GCAACTGTATTTCATACGTTCTTTTCAAAGTGGGATAGCTATTGCAGCTTAAAGAGGGGAGGGGT
Z18859	191 A C	;		CAGTACTGGTTTCCAA
	:			AGAACCTGACCAGATGTGGCTCGGAGGGGAATCCAGACCCGCTGCTGCTGTCTTGCTCTCCCCTCCC
				CACTOCTCCTCTTCTTCTCTCTCTCTCTCACTGCCACGCCTTCCTT
				CTCTGTGCTCTTCATTCTCAQGAJGGCCCGCAACCCCTCCTCTCTGTGCCCGCCCGTCTCTGGAAA
Z23091	159 GA	:	:	CTGAGCTTGACGTTTG
				GTTGGCATTGTTAGTAAAACTTCATAGGTGAAGAGGAGGATCAGTGAGATTAAGTTATTTAT
				GTGTGGTTTTCTGCAAGGGCAGGTTTGAAACCTGACCCTAGTTGTGCTCCAGGACCTA(AAGGCGTGC
				TCACTCTACCTTGTCTTTGTGTTGAAAGGAGTGGTTTCCCATGACTGTTTAAGTGACAAGTGCCATGG
11595b	125 A G	:: <u> </u>		ATATCTACACCGTCACCAGACTAGATTGTCTCAATGTCCTTGGCTTGCGAC
				GTTGGCATTGTTAGTAAAACTTCATAGGTGAAGAGGAGGATCAGTGAGATTAAGTTATTTAT
				GTGTGGTTTTCTGCAAGGGCAGGTTTGAAACCTGACCCTAGTTGTGCTCCAGGACCTA(AGGCGTGC
				TCACTCTACCTTGTCTTTGTGTTGAAAGGAGTGGTTTCCCATGACTGTTTAAGTGACAAGTGCCATGG
1159	11595 125 A G	1		ATATCTACACCGTCACCAGACTAGATTGTCTCAATGTCCTTGGCTTGCGAC
				TATATCACATTAGTATGTCACTGCCATGGTAAGGACTTTGATCACTAGGAAATAAGAACACTTTGAA
_				TGGTCTTGTCCTTTCAATAAAAAGAGTGACATGATTGAACATGTGTTTTAGATAAAGGGCACTTGAT
				IGCAGGAGTGTTTAGGATGAAGAGAGAGAGATTAAGGAAGATCAGGAAGAAGAAAGTAGCAATGGGA
124	1241 131 GT	:		ATGAAAATAGGAGGCCCTGAGATCCACTGGATAATCTAAAAAACCAAGAGAAAG

-				GTGOGATCACCACTACAGTCTAATTTCAGATGTTTTCATTACCCCTAAAAGAAATCTTGTACCATTA
				GCAATTATTCCTCATTCCTGCCCTCACACCCAGGCCCTATCATGATTGGCTTCATGATTGGCTTCATGATTGAT
1000	130 CT			ATETITICAAGGT
7071	2021			AGTATCACACATACTTAATATATAGATATACACAATAATAAAATCACTCCCTACCTTGAAAAACTTT
				AICHTAGAAGCATTTTTAATTTTACAACACAAAGCTCAAACGAACCTACAATAAGTCTAGTAGTCTG
				TTTACGTGCCAAGGGATAAGGCTGAACAATAAATTAACCCTTTAAAAATGTCTATGAACAAGTACAA
6810	68 C T			TTTCTTTTGAGTTCTGCAGAGCAATGACCACTAAGAAATATTTTAAAGGC
				CCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTATTTGCTTTTTGTAATCCAGTTAAGACCA
				TCAGCATATACAACATCATCACTAACTCAACAATGTAGCTGCAGGGTAACIACJTGTGGATACCCTG
				TETECTCTACTEGOCTCCAAAGGCATTCAGGGGATCATCAAAGATGTTGGACACCTTGTGTTCAAATC
6817	118 A C			TIGGITICAGGIGCGGCCTGTGCAGATCGGCTTTTGGTTTGG
				CCATTITATTITICTCTAAATTTAAAATAGAAGACTTTAATGGAAAACATTTAGTACCATCATGTCA
-				CCCTGAATGCCAGCAATACCTCGACTTTTACACACGCAGGAAGCCTAGTAAAAGCCCCGTCAGTAGT
		•		ACACATTICTCTATGGTCCTTCAACAGTTTTGCATATACAAAATTTTCTGCTATTTTGCTTTAGCAAA
6819b	212.C			CAGCAATAACTTTTGTGTTTCCTATATGACACCTAATATCCA
				CCATTITATTTTCTCTAAATTTTAAAATAGAAGACTTTAATGGAAAACATTTAGTACCATCATGTCA
		_		CCCTGAATGCCAGCAATACCTCGACTTTTACACACGCAGGAAGCCTAGTAAAAGCCCCGTCAGTAGT
				ACACATITICTCTATGGTCCTTCAACAGTTTT[G/T]CATATACAAAATTTTCTGCTATTTTGCTTTAGC
6819a	166 GT		,	AAACAGCAATAACTTTTGTGTTTCCTATATGACACCTAATATCCA
				CTGGTATGTCATAAGCAATCCATAATTGTTATAGCTATT[AVG]TTATACTATGGCACCATTTGGGACA
		-		CAGATTATATATGTCAGACACCACGAATGTCCTTTAAGATATGCAGCAAGCA
681xx	39 A G	-:		TTAACAAAAGAAATGAACGTCTAGG
				AGGATTCCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCTCCTTGTACCT
				CTGGTAGAATTCGGCTGTGAATCCATCTGGTCCTGGACTCTTTTTGGTTGG
		•		CACAATITCAGA(G/T)CCTGTTATTGGTCTATTCAGAGATTCAACTTCTTCCTGGTTTAGTCTTGGGA
6972b	149 GT		:	GAGTGTATGTGTCGAGGAAT
				AGGATTCCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCTCCTTGTACCT
				CTGGTAGAATTCGGCTGTGAATCCATCTGGTCCTGGACTCTTTTTGGTTGG
				TTGCCACAATTTCAGAGCCTGTTATTGGTCTATTCAGAGATTCAACTICI ICCIGGI I I AGI CI I GGG
6972a	122 A G	<u>i</u> _	:	GAGTGTATGTGTCGAGGAAT

			AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAGGAACTCA ATGAAATAAGCCGCTAACCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA
7598k	210 A C	;	ATATTTGATCCCATTATGTGAGAGATTTCCTGATATGTTATCTTATTTAT
			AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTA
7598j	208 A T	:	AIAITIGAICCCATRAGGGAGGGTITICCTGATAGTATCTTATTTTTCCGGTATTTCCT
		· · · · · · · · · · · · · · · · · · ·	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA
7598i	192 GT		ATALITICA DE LA COLONITA DE LA CAMBILITA DE LA
			AAAGGTAAATCAAAGCCGCTAACGATTTTACAAAAGAAAAGACACCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTA
7598h	144 CT	i	CCTCATGCAGA
			AAAGGTAAATCAAAGCCCTACTATAAATTATACAAAAAAAA
7598g	142 CT	:	CCTCAATGCAGA
1			AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTG(AGJGGATGCCTT TTAATATTTGATCCCATTATGTGAGAGATTTTCCTGATATGTTATCTTATTATATTTTCCCGTATTTT
75981	120 A G		CCTCAATGCAGA
		•	AAAGGTAAATCACAAGGTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAAGCTJCAGATTTTACCTTGGAGAAATGAAAATATTTCTTGAGGATGCCTT AAAAAAAAAA
7598e	83 CT		CCTCATGCAGA
			AAAGGTAAATCAAAGTICCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGC[C/T]GCTAACCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCTT TAAAATTGATCCCATATGTGAGAGATTTTCCTGATATGTTACTTATTTAT
7598d	77:CT		CCTCAATGCAGA

				AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAJA/GJAGGAAC
	_			TCAATGAAATAAGCCGCTAACCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTT
				TTAATATTTGATCCCATTATGTGAGAGATTTTCCTGATATGTTATCTTATTTAT
7598c	56 A G	9	-	CCTCAATGCAGA
				AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACGGCAAGCCAAAGGAAC
				TCAATGAAATAAGCCGCTAACCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCTT
				TTAATATTTGATCCCATTATGTGAGAGATTTTCCTGATATGTTATCTTATTTAT
7598b	47 CG	 G		CCTCAATGCAGA
				AAAGGTAAATCAAAGTTCCCTCTATAAATTĮA/GJTGATTTACAAAAGACACCCAAGCCAAAGGAAC
	_			TCAATGAAATAAGCCGCTAACCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTT
				TTAATATTTGATCCCATTATGTGAGAGATTTTCCTGATATGTTATCTTATTTAT
7598a	30 A G	···	:	CCTCAATGCAGA
				GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCCTATTCAGACATCTTGCCAGGTCTCCTGTA
79980	116 A T	:-	:	ATACTITAATGAATGGGTGTAGTCCTATCTTCTCAAGGTCCCCAAATAAAT
				GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCCATTCAGACATCTTGCCAGCTCTCCTGTA
7008h	94 4	94 A C	:	ATACTITAATGAATGGGTGTAGTCCTJA/CJTCTTCTCAAGGTCCCCAAATAACCTTGAGGTTCCT
2000				GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCCTATCAGACATCTTGCCAGGTCTCCTGTA
7998a	75 A T	<u>:</u>	:	ATACTTIJATIJATGAATGGGTGTAGTCCTATCTTCTCAAGGTCCCCAAATAACCTTGAGGTTCCT
				AAATACAGAATTTTATTTAGAAACTGTTTAAAGTAGAAAAAAAA
				AAAATGGGTTCCCAATAAAATGGAATTTTAGGGCAACAAAAGTCTAAAAGGCCQA/GJCAAAAGAGA
				AATAGCACCACTGTCATTTGAACAATGGCTAGTTACTTGCATTTTTTGGCATTGTTAATCACTGAATC
8071	8071 119 A G	:. ':		TGGGTTTTCCTCTGAATTCCACACAGAGCATGCACTACACACATTTTATCAT
				AAGGCTTTCCTCTAAACATCAGTCCTACGGAGAAACTGGGAAAATCCTGGATATTTGGCTTATCACTT
				TGACGCAAAATCCACTTTGCTGTAA(CTJGGTCATCCGAACTCCCTTCAGAGAGCAAGCAAAA
8467b	93 CT	<u></u> -	:	TTAAGTGTGATACTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAAGGAAAAATTACTG
				AAGGCTTTCCTCTAAACATCAGTCCTACGGAGAAACTGGGAAAATCCTGGATATTTGGCTTATCACTT
				TG/A/GICGCAAAATCCACTTTGCTGTAACGGTCATCCGAACTCCCTTCAGAGAGCAAGCA
8467a	70 A	 ⊡	:	TTAAGTGTGATACTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAAGGAAAAATTACTG
				AGGGITCAGGGTTTGGTTTTAAATCAGGCTGCACACCTTTCAAATCAATC
		_		AACTGGCTTCAGCTAGIC/TJAATACTTCATTAAATCGAAAAGAAAAAAATTGCTTTAAGGAAAAAA
				AATCCAGTTTTAAGAACAATTAACATTAGTCTTTAAAATAAAAGGAGGGCTAATGTTTCATGTTGCT
8498	84 C	84 CT	:	TTATACATCCTTCTCCTCAATACAGAACCAGGAATGTAATTTTCCTAACTCAG

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			CTANGGANANAN TANGGATAGTTTGGGATAGANTAGANCTANTGTTTACANTGATTCTTACATT
			TAGCATTAATCAGAAACGA
WI-18562 2	29 GA		ATARCAGACTITITAATCAATGCCAGAGACAAAGTGAGGCCGAGCTAAGAAC(AC)CGCTCAGCTTC
			TTACAATGAAGAAATGGTTTCCTTTCGATGCAAAGTATAATTGTAAACCACAGIGCICGCACAGIIC
	<u> </u>	-	AC
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				ACAGATGTCAGTTGTTTGAATTGGCCCATTAAAGTATGGGGCTTTTCTTGTTAAAAAGTCATTCCAAA
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				GECCCCCGGCAGTCCAGTCCAGCGGGGGGGGCTGCCCGTTCCTGCCAGTTCCTCACTTCJGCGGGG
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				GTTTGCAAACCAACATGTGCTCTTTCAGTCATTCACTGTTTTAATATGACATGGTAGAGAAGATAAG GTTTATGGCAGGTAATTTTTTGTAATGTGTATTAAACGAAGTTCAAAGATTAGAAATACATCTGTGTC
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				GACGTGGACAAAGGAGGTTTAAATGAATACTTTGTTTGTT
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				TGGCCTCAATGACTGGTACATTGGAGAAGCTGTGCAGCAGCATCCTTTTCTGTGGTGGGCAGGGCAGG AGATGAACCATAGGAGCCAAAAGTC WG GACAAACAGAAGAAGAAGAGGCACACCAAGCGTGAAACCTC AGATGAACCATAGGAGCCAAAAGTC WG GACAAACAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA
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				TGGCCTCAATGACTGGTACATTGGAGAGCT[G/AJTGCAGCAGCATCTTTTCTGTGGTGGGCAGGGC AGGAGATGAACCATAGGAGCCAAAAGTCAGACAAACAGAAAGAA
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		-		CTTCCTCTGTTTGGCTTTGCATTTGTGCAAAAACCACTTGGAAGAGGAGTTTCCTGCAA AACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCGCCCTTGACTGAJC/GJAAAGC
WI- 20512d	126 C G	<u>;</u>	ı	TTAGAAAGGAAACTGAAATTGCTTCTTTGAATATGGATTTTAGGGCGGGC
				CTTCCTCTGTTTGGCTTTGCATTTGTGCGATTTGGAAAACCACTTGGAAGAAGGGACTTTGJTCCTG
WI- 20512c	29 ⊥	9		TTAGAAAGGAACTGAAATTGCTTCTTTGAATATGGATTTTAGGGCGGGGGGTGGGT
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			CACTCAAATACTGGAGCATGATCAGCAATAAATTCTATTCCATAAACCAGGTAGATAAATGTCACA GCTTAAAATATAGTTAAGTACAGTTGATCCTCGTTATTCATGGATTCCGTATT
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		_			CAAGCCCTTCTTGGATTTGCCTTCATGAGAAAATGGTGGCTTGGGATGGAGGTGACATTCCTTGCTGT
					GGTGAACTGCAAAGAAGGAAACCAGGCAATGTATTCCATAGAGGCCTTTAAAGAAGACCCG[T/C]TGG
	WI-19307 1	196 T	:	•	AAATGGGCCATGGTCTAATTTGGTGTTGAAATAAACTAACCTCTTTGGCTG
					CTTICCCTCATCCCTCTTCCACCACACCATCCCGGAACAAGTGCTCCAGGATTCCCTGCCCACTGGC
					CATTTGGAGTGTGTCC/A/ITTGGGTAGCAATGTGGAAACCACCAGGGCCTTIGTGGAAAAAUGG
	-				AGGGGGTTGAGGGAGTCOCAGGAGGGGCTTATTGAGGGCCTTTGCCACTTGCTCATAGGCGAAGCTCA
	Wi-19269	85 A		:	ATCTCCTCATCATCTGGACAGGTGGAAGCGAATTCTTCCCGGGGGGTAGGCA
					CAATGGACTGAATGAGTGCGTGGGTGGGGGCACACACACA
	•				CTTCCAGTTTTAGAAAACAGAAATCTGCATCTCAGCCTGAGACGCACAGAGAGGTJCTTCCTG
					ACCCAGACGCACTCACGAGGCCAGGTCCTGGTTTTCAAAACTGCATTTAACCTGCGCCAGAGAGGTTCAC
	WI-19946	122 C	1		CGTAGGCATCTTTAATAAACTAACTCCAGCAAAATGTGGGTACGGTTACTAA
					CACAGCATGGTGTAAATAGCATCAGATTGAATGAAAAGTTTGTTAAATGCAACCATAAATAA
					ATAAATATACATCAAGTAACTTTACAGCACACATTITTTAGGGCCAAGGTTTGGATCTGTCTGGACCT
					CAATGTIG/AJCTCTCGGAGAAGCAGCCACGTTAGCAGCAGATACCTTACAGCTTGTCATCTACTAA
	WI-19956	141	·- V	:	GTGATGGCCAACAGAAGCTTCTGAACTCCTCGGGGGGGGTAGCTGALAAG
40 GA 26 T C 154 T G					TTGGTTGGATACTTGCTGGAAAAAAAAAAAGCAGTTTTAATTG/AJGTATTCAAAATACCTTTAAAAA
40 GA 26 T C 154 T G	_				GTATTCTAGCACAAGATTTTCTGTAAACTAGATTATGTTGTAAACTTTTTTCTAAATCTTGTAGAACTTTTTCTAAATCTTGTAAACTTTTTCTGTAAACTAGATTATGTTGTAAACTTTTTTTT
26 T C					TGTCGGTTGTTAAGAACTAGAGCTTATTCCTATTCCAAATCTATCT
26 T C	WI-19076	40 G	Α	:	AAGGCACTTGAAAGCTGTTTCTTTAAGATATGGGAATTTCTTTTTTTT
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26 T C 154 T I G					AAAATAACATAAATTGGAGGGAACAGTGGGATGCAGAAAGAA
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154 TIG		-			CAACCTTTTTGACAAGGGGACGTGAATTTCTGATGAAAGTTATCTTACCAAGTTTAAATTCATAATTG
154 TIG					GGAATTCCTCTTTAATATCTCCAGGCTTGATTGGGGAGGGGGCTGGGCTCTACCCTTTTAATATCTTCTTGATTGGGAATTCCTCTTTTAATATCTTTGATTGGGAATTCCTCTTTTGATTGGGAATTCCTCTTTTGATTGGGAATTCCTCTTTTGATTGGAATTCCTCTTTTGATTGGAATTCCTCTTTTGATTGGAATTCCTCTTTTGATTGGAATTCCTCTTTTGATTGGAATTCCTCTTTTGATTGA
154 TIG					TCCAGTCTATTGCCAGAT/GCCAGAGAAAGCGCGGGAAGCCCAGCTCTCAGCATAGCCACTGTGGGGAAGCCCAGCTCTCAGCATAGTCAGCAGCAGCGCAGGAAGCCAGCAGCAGCAGCAGCAGCAG
	202959	154 T	ig	::	GTGGGCTTCACCTTCTGTGGACTCCTCATGCTGGGACTTGTCTTTCAGGG

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				CTGGGAGTGCTGACCTAAGTGACATTTTTTTTTTTTTTT
Wil-	000	1	•	CAACAGTGCCACAGCTGAGAGGTTCCCTATACTTCCTACTGTGTGACAATTTAGC(G/A/ATCCTTC) AAATGGGAAAATTCCTAACTACAGAGAGAAATGGGTCCTACAGTAGGGGCCG
	7			GAGCCAAACCCAAAACAAAAATAAAACAGAACTCTTTTGTAAACTAAGTCATACCTACTTCTTCTTCTTCAGAAATTAAGTTCATAAAACATGATTTTACAACATGAAAAGAGGAGGTAGGCATAATTGTTCA
	,			AATTICATCTITICTCAAATTITAAAATTGTTTTAATCCCAAAGGTGCCTATTGAATTCTTCAAAAATA
Z/502-IM	0 ×			CATGACAAAAGACAAAGATCAAGGAGTAACATAAATTATAAGTTGAATAAATA
				TTCACTTTTAAGAAAATGTGAGATCCTTTGTTGGTTTTTTATTTCCTTAAGTACAAAATGCTAAAC
WI-20588 133 GA	133 GA			GANGGARGACON CARACTOR CONTRACTOR
				TGACCTCATACTGGGTTCTGGTTAGAACACACACACACAC
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WI-20593	79 A G	- (6		CCAGAAGCCATTCCATGGGGTATTTGGTCTGCATACTGTGAGACACTGAGCT
	-			TTCTTTGCCAAGCCTGTTCTTCAAGTTATTCAGAACTGGGTGTATACCTTGTCCTCCAT/C)ATGTATCT
				TGTCCCTGCTGTTTTAGGTTAGCAAGGTGTATGAATACTTTTAGGTTGTTAGGAATACTTTTAGGTGTAGGAGGTGTATGAATAGAAGGTGTATGAATAGAAGGTGTATGAATAGAAGGTGTATGAAATAGAAGGTGTATGAATAGAAGGTGTATGAAATAGAAGGTGTATGAAATAGAAGGTGTATGAAAGAATAGAAGGTGTATGAAAGAATAGAAAGAAG
				GGTATCAGTGAAATACTGATCTATTCTCTGGCTAGGGTCAA! ACAAAA GCCA GGAACTGACG
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	_			TGACAAGGGAGAGAAAATTCIACICAIIGCAAGGAAATCTTCTTAGCAGGAACTGG
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				TGACAAGGGAGAGGGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCAC
			-	AAGCACTTAAAACCCATGAACCTTCAGCTGATCGTCCTTAGCCAGTCCCAATCTCTACGAGGAACTGG
*				CATATGTTCTTGCGTTGGTCACCCTGTAGCTGAATTACTTCTCCATATICICALIGAAIGCICAAIIAC
	184 CT	T		AGTACCATTGCAGGCAAACTTTTCTTAAACGCCTTCACIAGITICTITIA
				TGACAAGGGAGAGAGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTICAGTGAAGCAAC
	_			AAGCACITAAAACCCATGAACCTTCAGCTGATCTICTTCATATATACCGATGATATACC
				CATATGITCTIGCG[T/C]TGGTCACCCIGIAGCIGAAIIACIICICCAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIIACIICAAIICAAIIACIICAAIIACIICAAIIACIICAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAAIIAA
WI-19066# 148 T C	148T	ر د		AGIACCA I IGCAGGCAAACTI I TOTTAACCOCTI CACTICOTI

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			TGACAAGGGAGAGAAGGGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAAGGAAGTGGAAGAACCCATGAAAACCCATGAAAACTCGAGGAACTGGATCAATCGTCTTAGACAGTCCAATCTCTAAAACCCATGAAAACCCATGAAAAACCTTCAAGAAAAAAAA				
*			CATATGITCTTGCJGCTTTGGTCACCCTGTAGCTGAATTACTTCTCCATTTGCGGATGCTCAATTAC				
190669	147 GC	:	AGTACCATTGCAGGCAAACTTTTTTTTTTTTTTTTTTTT				
			TGACAAGGGAGAAGGGAAATTCTACTCATTGCAAGGAAATCCTCAGTTAAGCTTCAGTGAGGCAC				
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T			TGACAAGGGAGAGAAAAGGGAAAATTCTACTTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC				
			AAGCACTTAAAAACCCATGAA(C/T)CTTCAGCTGATCGTCCTTAGCCAGTCCAATCTCTACGAGGAAC				
W.			TGGCATATGTTCTTGCGTTGGTCACCCTGTAGCTGAATTACTTCTCCATATTCCGGATGCTCAATTAC				
1990	87 CT	;	AGTACCATTGCAGGCAAACTTTTCTTAAACGCCTTCACTAGTTTCTTTTA				
-			TGACAAGGGAGAAGGGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC				
_			AAGCAIC/TITTAAAACCCATGAACCTTCAGCTGATCGTCCTTAGCCAGTCCAATCTCTACGAGGAAC				
	-		TGGCATATGTTCTTGCGTTGGTCACCCTGTAGCTGAATTACTTCTCCATATTCCGGATGCTCAATTAC				
19066a	72 CT	:	AGTACCATTGCAGGCAAACTTTTCTTAAACGCCTTCACTAGTTTCTTTTA				
			TTTACAGCGAGTTTTTCCCGTCTCAATAAGTATGAATCTAAATAGATTAGGGTGAAAAAGAAAATGTG				
	-		TGTCTAAATAAAATCTCCCTTTTTGAATGTATATTTGT[G/CJTTAATAAAGGGAAGCAIIAAIAA				
			CAGACATATTTACAAGGTTCTGAACATGAGTGATTCCATTACTGTTTTCTGTACAAGATAGAACAAA				
WI.20660 105	105 G C	:	AAGCTATCCACCCGCCCCAAAAATACTGTTTAACAACACTATGTTTTAAGA				
			CTISCTISCOCASCTTCTCTTGSCOCTGCTCOCAGATGSCOGGTCTCCTGSCAGCCTCCCCTCAGTCTTCC				
			TOCADOCOBOCTICOTTCOCAGOCTGCCTGCATGCATGTGCACCTTGGT[C/I]TTCGCTCCATCGCC				
WI-18768	120 CT		TTGAAAGCTCTGAA				
			TTCCCCAGGGTTCTGTATTGCAGCTAAGCTCAAATGT[AAGJTATTTAACTTCTAGTTGCTCTTG				
			GTCTTCTTCCAATGATGCTTACTACAGAAAGCAAATCAGACACAATTAGAGAAGCCTTTTCCATAAA				
			GTGTAATTTTAATGGCTGCAAAACCGGCAACCTGTAACTGCCCTTTAAATGGCATGACAAGGTGTAA				
78001.1W	37 A G	:	AGTGGCCCCATCCAGCATGTGTGTGTCTTGTTTGCATCTACCTGCTCC				
-			GAAAGCCAGAGATTAGCCCCGCATTCCGCATCTGTCAACCAGGACAGAAATJGCATGGACAAGGGAA				
			TGAGCTTTACAAAGATGATGCACTTTGGAGATCAGAAAATTCATATTTAAGCAAAGIGATACAAACA				
WI-18790	49 AT		CAGTGATTTGGGAATGCCT				
		:	AGGAGGCTGTTCCAGGAGTCCTGCCAGCAGCCTQGAJGTGGCCAAGCCCAGACACTCACCCACTT				
			COCCAGTGGCCCCGTGGATCCTGGTCCTAGGCTGGACACAGGGATTCAGAAGACACCAGGCTGCACA				
			GAAAGAGCCAGATGGACCTGAGTGTCGGTCACAGCCCCCTACACICAAGGCTIGAGAGGCUTUAGGAA				
WI-18987	35 G A		AGTCA				
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					TGGATGAAACCACAGGGATTCCGGACTJGCCAGACCCCATTTTAIACTTCACTTTTCTCTACAGTG
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WI-18919	26 CT	-			GGGCTGAATAAA
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¥.		:			CTTTCTGGTCAAGGCTTTGGACA[T/G]CTCTTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTCG
18741a	23 T	ত		:	CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAATTTTACAAGCCTGGATGAGGCTACTGA
					TCAGAAGCAGACATGGCATCTGTTGCTTGCTTGTTGGTTG
					TTAGAATTGCCCAGTGCTGCCAGAGTGAGTGAGTGTAATTCTCCTTTCAGGTAAAGATAGGCTATCTC
\$	-	-			AACACTGCTGAGTGATTCATAAACATATCAACCAGAJIAGCATTAACCCATTTTATTTCTTTTAACATAACATAACA
19179a	170 GA	등	-		AGIGICIGAAGAIGCICAACAAGIIIICIGIGIAAAGIAAGGAAGAAGAAGAA
					CCAAGTTGCATCCATGTTTGATTTTCTGATGAGACTAGAGTGACAGT/AJGTTTCAGAACCCAAATGT
		_			CCTCAGGTAGTTTGGAGCATCTCTATGAGATGGGATTATGCAGATGGOCTATGGAAAATGCAGCTGC
		_			ATAATTAACACATTATCAAAGTCCTCTTACAATTTATTTTCCGCAGCATGTCAGCTAAGTAGACCCA
WI-19212	46	Ŧ	-		ATGGGGAGAGAAATGCCTGCTTTCTTTCCCTCTTTTCTGCACTGCCATAT
					CTGTTGAAGGCTTCCTCAGGCAAACTCCAGCTTAAAGCCCTAGACAGGTAAAAGCACACATTGGATG
		_			GCAGCATGGGTTTCTTCCCATTTTATGGGCATGAAATATGTGGTTTAGAATAAGGAACAAGCATTATT
					OCTITIGOCAACAGOCTCACTCTAAGAGGCTTTTTTGCTGAGTCAAGCAAACACTTGOCTGCTCTGCCC
WI-19183 210 GC	210	2			CTTGGAGGCFTGCATTGACCTGCTCTCACTGGTAAGGTGACTTGGTGGC
					TTGAAATCCCAGTCTCCTGGCCCCAGGCAGGGTCTGTCACCATAGAATGTCTTCCTCTACTGGGGTC
					GTICTGGCTTTTTGTTAGAAACTTGGTCTGAGATGTTCTTCCCCTGTCCATTACCATTCGATGTTCTT
Α̈́					TGTTCAGAGCAATGTTTCTTGTATTCTGAAACTGGAAACTGAACCAGTTTGCCTTTCTCCTAGTCACC
20014b	214 T	<u>C</u>	•••		AAGCATACTĮTICCTGGCTCCCCAAGTACTTAAATGTTCTCATCTGT
					GTCTCCCCAGAGTGCTTCTGCACCCCAGCCCCTGTCCTGCCTG
					TCTCTGCATCCCTTCCCAGGGGGGGGGGCCTTAGTTTGGACATGCTGGGTAGCAGGACTCCAGGGGGGTG
					CACGGTGAGGAGATGAGGCCCCAAGGTCATCACACCAGGGGGCCATCCTTCTCAATACAGGCTTCJG
WI-19041 198 T C	198	<u></u>		;	COCTTGCAGTCCCTATTTCAAAATAAAATTAGTGTGTCCTTGCCTGTCTGT
		-			CAGTTACCCTGCTTTGCCTCGAAAAAGTGTCATCAATTTGTAATTTTAGTATTAACTCTGTAAAAGT
		_			GTCTGTAGGTACGTTTTATATATATAGGACAGACCAAAAATCAACCTATCAAAGCTTCAAAAACT
					TTGGGAAAGGGTGGGATTAAGTACAAGCACATTTGGCTTACAGTAAATGAACTGATTTTFATTAACT
WI-19135	20 GA	<u>₹</u>			GCTTTTGCCCATATAAAATGCTGATATTTACTGGAAACCTAGCCAGCTTCAC

				TACACAGAGGGTCGCACTTGGACTCTGAGGGTTGGGAAGGGGGAAAAGGGGAJGATGGAGAC CTGCTCCCCAGGTCTTCCTGTCAGCCGGTTTACATGGGAACAGGGTTAACATCTGTGTTAGGGGAGGT CACCTTACCCTTTTCATAGGGGAAGAGTGTCACACTCCTGGCTATCTCAGGGGAATGGGGAAAAAAAA
WI-19236	54 GA	-:- V		AAICIII LAAGAGAAAAAAA COO COO COO COO COO COO COO COO
				GIGCCAGICI ICCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA
				ACAGGAGACCCCTTTGCAGGACTTGCACACAGGGAGGCTGTAGCCAGGAAACCCTCTTCTTCCTGGT
WI-19144 222 GC	222 G	 C		CTGGCTGGCTGGAGCGGGCTTGGAACACACTTCAGTGCTGGTG
				CCCGTCTAAGGGAAAAGCTAATGTTTTCCACAAGACTGAACAACGACGTGTATTTACACGAGGGGTAAC
		•		GGCAGATGCCTGACAGAGAGAGTGGGTTTGGCAGACAACAACACAGATTTGTGTGAAGCCACCAGGGTGCTTTTGG
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				CCCGTCTAAGGGAGAAAGCTAATGTTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGA
				C/TIGGCAGATGCCTGACAGAGAGTGGGTTGGCAGACACACACA
- N				ATGGGTGTGGCACCTGGACGTGTGCAGCATGTGGCGGTCTCTGTGTGAAGCCACCGTGCTTCTTTGG
19139a	66 CT	<u>-</u>	:	GGGGCCGCGAGATCTAGCATCTCTGAAATCCTGGCTGTCGAGGCTTTGAAG
	-			GGCTGGGACCTTTAGGAAAGTGAAATGCAGGTGAGAAGAACAAAACATGAAAAGGAAAGGGTGCCT
				CATCOCAGCAACCTGTCCTTGTGGGTGATGATCACTGTGCTGCTTG[T/C/GGCTCATGGCAGGAGATT]
WI-18910 112 T C	112/7	- - - -		CAGTGCCACGGTTTAGG
	-			TTCAGGAGGTGGAGTTCGTCGTCAGCTCTCCTGCTGTGATGTGGAAGCTTCTGATATTTGAAGAAACA
				CGAATGICTCTGTAGCTTCCTCTTCACTGCCCCAGTATTGCTCTGTATTATCAGCGATGCCTCTGT
				CACTCATGCCTTGCCTAATTGTTCACAATGGTGGAAJA/GJGCTTCATGTBATGATGATCAGGAACAA
WI-19235 173 A G	173 A	9	:	TCCAGTTCTTCTGAAAGTGTGACAGTGTCCAGCCGGGIICIGCAGCAACIA
				CGTTTTCOCTAACTCACCCAGTTTAGTTTGGGATGATTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT
		· ·		CTTGGAATTGTGAGOCTCTATGTTTCTGTTAGGTGAGTGTGTTTGTGTGTGTGTG
				GGCAGCATCCCTCTCTCCCTAAAGGGACTCTGCGGAAQCTJITTCAUACULULIULUAGGAAC
WI-19222 179 CT	179(TC		GGGGCAGGTGTGTGTGGTACACTGACGTGTCCAGAAGCAGCACTTT
				AAATAATGCAACGCAGGAGGAGAAAAGAAATGCACTAAGACAAGAAGAACATTCTCTCATAGAACATTG
	_			ATCTGTTTTACAGGAAACAAACCTTGCCTTGAAATTTACACAGIGAGACIGIAAAIIGCATGAAA
				A/A/G TAGCTATTTTTTCCTAAGACATTTTCATTCATGAATATTTCAAGITTTTCATAAGAATATTC
WI-19117 134 A G	134	٩	:	CATTICITAAAACACATGATACCAGCAGCAACIGAAAAIGAAIGAAIIGAAAIGAAA

				CTCCTGTTCGTGACCTGACAGGGTGACACAGCCCCTTTCACACTCTGTCCTCCTATCTTCCTGGGTAGA
Ś				TGCCCTGGTGTAGGGCTGAGTACTGAATGGTCTTCCALCXXXAGGGGGGGTGTGTGGAGTGGAGTTTTCAGAGCAGGTTGAGAGCAGCTAGAGCAGGTGGAGTGGCTAGGCGTAGAGCAGCTGCAGCTGCAGTTTTTCAGAGCAG
34c	263 CT			TTCATCCACTTGCTCCTCCTCTACOCTCGGCACCCTGGGTGGGAAAGGG
				CTOCTGTTCGTGAOCTGACAGGGGTGACACAGCCCTTTCACACTCTGTCCTCTTTTCTTCTCTGGGTAGAGGGGTACTGCTGGGGTAGTGGTCTTCCATCCCAGCAGGGGGGTGCAGCAGGGGTTACTGATCTTCCATCCCAGCAGGGGGGTGCAGCAGAGGGGTTACTGATCTTCCATCCA
				GOCCTICABAGCCAGGGCTAGAGGATIC)GCACGGTGGCTAGAGCCAGCTGCACTATCCTTTTCAGAG
19134a	162 T C			CACHCAICHGCICCICCICCIACCICGGCAACCIGGAAG
				GGTTTCACCAGTCTTTCCCAGGGAACTCCGATGAAGTGTTCCAACAAATGAGCGAGTGAACCAAGA AGAGGATGACATTAGATCCAGGAGATACAACAGAGGAGATAATCTIC/TICAGGATGCCTGTGAAGA
				AAGATCCCTGGATCCCAGGATGATTATAGGACAAGTTGTTCATAATCCAGCAGGOCAGAAGACTTCC
WI-19224 112 CT	112 CT			AGGGAAACTCCATCCAAGGAGGTGAAAATGATGGATGACTCCTCCAAGATGAAAA
				GCAGCTCCTAAGGACCACTGGCCATTAGCTCTTGCTTTTGATGGCATTCTCTTTCCACCTTGTCTTCTC
				CTTTGCTCCTCTGTGTTAGTGTGGCAGGTATGACAACTCATCCAGTGGAAACACAGGCCTCACACTGCC
				CTTCCGCCCCCCCCCCTTTGCCTGCAGGTGCACCGAAAGGACTTCTTGGGGGGATAAAATTCAAAAAA
WI-19201 179 T	179 T C	ر د		GTGTGATGTGCTCAGAAGGTCAGACTCCATGTCTGCCTTGGCCTCAA
				GAAATGGCTCCACTCAGAGCTACCCCGGTGATGAGGATAGGGGAA[I/C]ACTTCTATTACATTAAAG
***				GCAACAGCAGTTAGTAAAAAGGTTTTTACAGTGTTTCTGCTGTTTGAAAGTGCAATATAAATTTTTG
				CTAGCCCATGATCAATCGACTTCTATTGTTTGATATACACTTCAGCATTTAAGTTCTGTCGAATTGAC
WI-19034	45 T C	::	:	ATTIGCTACTIATAAACTTAGTCCCTAAGTCTTCTTATGCTGTGCTATATA
	_			TGTTCCTGAGTCACGCTGAGGAGAGGCGCTTCACTCAGGAGTTCATGCTGAGATGATGATGAGTTCA
				TGCGACGTATATTTCCTTTGGAAACAGAATGAAGCAGAGGAAACTCTTAATACTTAAAATCGTTCT
				TGATTAGTATCGTGAGTTTGAAAAGTCTAGAACTCCTGTAAGTTTTTGAACTCAAGGGAGAAGGTAT
WI-19102	25 C G		1	AGTGGAATGAGTGTGAGCATCGGGCTTTGCAGTCCCATAGAACAGAAATGGG
ż				AAAGGAGGAGAATCTTTTTACATAAATGCCTTGCATCATCCTCCAGTCCCTCACTGGGGGAA(A)
18548b	65 A G		:	GIAAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
ķ				AAAGGAGGAGAAATCTTTTTACATAAATGCCTTGCATCATCCTCCAGTCCCCTCACTGGGGGAJA
18548a	62 GA	<u>:</u>	:	AAAAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
				GGCAGCAGCTTTTTAATTTGAACACTTTCTTCTTGAGGACACACCTTCAGTACAGTTAACAAATGGT
				TACACCTGAAATCTGCTGAGAGCAGAGGT[T/C]AAGATCCACAATTGCAAAGGCCACTGCTGGCTCA
WI-18700	97 T C	 Ö		СТТССТСАСА
	<u>L</u>			CAGAGGGAAAAGTTTATTGAGTCAGCCACAGAGGAACAGAGAAACAGACACAAGGAGGTTCTGTGT
				GCATGGAGGAAATCAGGGCGCCGNACAGCTGAACCCTGCGCAGGGACAGAGGGGGGGGTTGGGACAGCA
WI-18501 121 CT	121 0	:- <u>-</u> -	:	GCGCATGCCACAACATTCA

				ACAAAAGAAAATGGAAATAGGTTTGCGAAAACTTATCTGCATGTACAAGTAATCCCCGTAGATAA
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181181	401	; ;	;	GTGATTTCAGAAACCNTCGATTCTGAATATCCC/A/GJTGGCGGCATATGCAAAGGAAGATGA
	2			TATACGGATCATGTATTTGTGTGACCACCACTACCACAGTCAATTTGTAGAGCAGTTAAATCACTT/C
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WI-18254	64 T C	<u></u>	:	TCCGTTCCTAGACATTT
	-			CAAATGGGTGGACTGAGTGATAAAACGCATATTGAGAACAAGACGGCCTTCTGGCCNCTCTGCGTCC
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18265b	117 CA	A	;	CTTGGGTGGTTCTTCAG
				ACCACACATTIGTTGAGAGCCTATTGTGGAGAACAACAGC/JTTGGGAAGTAAAGGTTGATTACT
WI. 18205		40 CT:		TCCTCTCCAAGGATGATATGTTTAATGAATTCCCTTTNCCTTAGCTTCATCTTCATAATGCCAAA
200				GGGCAAGAGAGAGAGATTTAATTGAATAAAAACTCCAGGCTGTGACACGGGTGGGAGACACAAA(T/
15				CIGAGTAATTAACAACATAATTTTANATGACAGTGCAATTAATTAACGTCCTGGGTAAGCCAGAG
18450h	FAT	64 T C		GGGGAGGAGGCGTCTTCA
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				GCTTTCATTTTCTGTCACCCACCCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAACAT
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				CATATATAAATCTATATCATATATATACACACAAACACATTCTACCAGCACTGTGAAGACACAGA
×				CTAGGCTTTACTAGGCTTGGGGCCTCTCCCATGCCACTTAAAAATGNGCACAGGIIIGCICIAIGCAA
20116c	59 T A	A		GAATTTCAACAGAGTTGGTCTGGGCCATCAGTCTGCAATTTCAACAGAGATTCAACAGAGATTTCAACAGAGGTTGGTCTGGGCCATCAGTCTGCAATTTCAACAGAGATTTCAACAGAGAGAG
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				CATATATAAATCTATATCATATATATATACACAACAACAA
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20466b	133 GA	V	;	ACAGTAACACTACIIIIAIIICIIIGCICIIIIAIICCIIICAGTICAGGGGTAACACTATTICA
				CTGGGCAGCAGTAACCATTTTAAAGAAATACTCTCAACAAGAGIICIIIIIIIAIGAGGAAGAATATTTA
				GTTGTTAACAAAGTTAAAATACTTATTGGAACIAAIICIIIGIAIIIIAIIUGAGGAACAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG
WI-21444	39 A G	J.G		ATAAGATTGACTTACTCATTGITGACTGGTTTTTTGAAGACTTACTGAGACTTACTGAGACTTACTGAGACTTACTGAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAGACTACAACACAACAACAACAACAACAACAACAACAACAAC
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21034b	148 T C	0	•	GAGATTBBATTCJGCCTAACCTATCTCAATTTTAAGTAATGTGAGCAA
				GGCGTGTATTTGATGCAATGTCCAACCAGTCAAGCTATCATTGAAATCCAAATATTTCCCAGTAATTTC
				ACATGCAGAGCAATGTCAATGTAACATACAAGCGTATTACCICCCCCIIAAGIGAACTGAATTAACTTGAGGGCA
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21609b	146 GA	Š			

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21609a	42 C T			THE CONTROL OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF
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12a	104 T G	ا ھ_۔۔۔	:	CACATTTCCCCCACGTCTAAGGGCAGGCAGCTACACTTGACTGCA
			٠.	ATCGGCAAGCTACAGCCTTAAAATCTGAGCTCCTCAAGTGCACAATTTCTGTGCCCTTTAAGGGCGCAATCTAGGGGAATCTAAGGGGAATATGAAGGGG
				CAACACTAAAGATTTCACATGAAAGGGCCGCGGATTGATT
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710500	2			ATCECCAACCTACACCCTTAAAATCTGAGCTCCTCAAGTGCACAATTTCTGTCCCTTTTAAGGGCTCA
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210288	121 AC	 A	:	TACGG
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×				TCATACAAGACAAGCACACACCACCAIGCCICIGAGGAACAIIGAAGGAAG
18829d	58	58 A G	:	AA
				ACAACATGCCTGTTCACAGGGGGAAAAATCCTAGGTI/AJAATAACTTATGTGTACTICTIGATITUA
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18829b	35	35 T A	:	AA
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7000	,	- -		AAGATGTTAACAAAACAAATTAAGGCTGCTGGGGAAACCTGAGTCCATGTTAAGCTTG
WI-20304	ò	5		CTCTGAACTAAAGGCCCGTGAAAGGCATGATTGGTTTTGGCACACAGAGTGGATAACCATTAAAA
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Š				GTTCTGGAGAAAGTTAAAATAATTACAAAGACTGACATGCAACTCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCCTTACCTTACCCTTACCTTACCCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTACCTTACCTTACCTTACCTACCTTACCTTACCTTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCT
20059a	59	T A	:	CATCTACAGACTATTTTCTCCCTTAGGAGATGAGGAGTATGGGGCTTAGGG
				TGTTTTGAGGGCTGTAGCAGACTACATACATGAGGGGGTGAAAAGCGGCTGCCTTCCTT
				CAGCAAGGGGAAAAACAAAAAAAAAAAAAAAAAAAAAA
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22130b	165	165 C T		

				GCTTAGTCTCCACCCTTTTAAATGTACTCTAGGTACAAAATAAACATTATACACATATAAGATCAGTCCTTTCCAACTTTTAAAATAGCTTTTAAAAAATGCJTTTAGTCAGGAGTCACAAAAACTGTCCAAGAAAACTGTCCAAGAAAACTGTCCAAAAACTGTCCAAAAACTGTCCAAAAACTGTCCAAGAAAACTGTCCAAAAACTGTCCAAAAACTGTCCAAAAACTGTCCAAAAACTGTCCAAAAACTGTCAAAAACTGTCCAAAAACTGTCCAAAAACTGTCCAAAAACTGTCCAAAAACTGTCCAAAAAAAA
WI-21661	117 GC		;	GA
				TCAGTTTAAACACATTCATCAAGGA[T/C]AGATTAATTAATGTCAGGTGAGCATAAAAGGGAGATTA
₹				TAAACCAGAAATGTGTTTTCTGGGAACCAAGTTTCAAGTGACTCAGGATAAGTTTATTAATTTTCAGTAAAGTTTAATTTTTTTT
21980a	25 T C		:	GGGICAAGCCCCIGGGAIAAAG
				TGCTTGTATTAATGTGGTGTTTACATTATCCTATTTCACAGATGGAAACAGAAAATACCAGCTTTTT
			-	AAA[A/G]TAGCAATATCTATTATATAATAATATTGAAATAACACCATAATATATAT
		•	•	AGTAATCTAATTGTGTTGATTTTGCAGAGGAGAAAAACATTACCTCTAGAGCTGAGGCTATTGTGC
WI-21636	7.1	71 A G	:	TCATGCAAACTCCAATCTGAAGGTGGTAGAAACTAGGAAGGGGACAGGGATTTC
				TTGCTATAATTTCCTTAAAAATGCAAAAGAGTACATCACAGCAGAGTATAGCCAATCACTCATTAGA
				CAAACAGTAAACATACTGGACACGGTTTCAGGCATGAAGGATACA(G/A)CAGTTAATTAACTAAAG
ż				GAACAGAGTCCCTGCATTCCTGAAGCATAGGATGGGGAAACAGTAATGCCAGATTAATACCTGGGGCC
57a	112 GA	V	:	AAAACCCACTGAACTCACCCCAGCTGAAACACTGAAGGATACTGGGTAAGGA
				GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAATAGCCTGATGTACGACCTTCGCGTCATACTTAT
				AATGGTTAATAACAGCATTCCTGTCTACCC(C/T)GATGATGCTTCTCTCTGCAAATGGACTATTTGCC
×				CAGTTGCAACAGGGCTAAGATTGTCGCACTATGACAATGAGTTGTTGATTGTTTGGAGTTGCGGTGTC
21524b	97	C1		CTGTCAGAAAGATTTCTTGACTTCTCCAAGTTACTTCCTTC
				GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAATJACJGCCTGATGTACGACCTTCGCGTCATACT
_				TATAATGGTTAATAACAGCATTCCTGTCTACCCGATGATGCTTCTCTCTC
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21524a	35/	35 A C	1	CTGTCAGAAAGATTTCTTGACTTTCTCCAAGTTACTTCCTTC
				TTACCTTCCAAACCAGGCCACTTTGGAGAAAGGG/TJAAGAGAATGCTATTAATCAATAAGCCAAGAC
				AATAGGGACTACCTGGGGTAGACCAAGATGGGCAGTCACCATACACCATCATTOCTGCCACAGAACC
\$				TTTGCACATGCTGCCCTCCCTACTCCGCACTCACCTGTCTAATTGGGACCTGAAGCTTCAGCATCCCTT
22652a	32 GT	GT	:	CTTTAGGG
				CAACAGGCTCATGGAACAGAGCTAGGGATOCAGGAGCATAGGAGGTGGTGGTGCTGGGCAGGGCTC
				TGCATCCCCTTTCCTCAGCACAGCACCATCTTCACCCTCCTGGGAAAGCAGCATTGGAGCCTACACCA
Š				CTTGTGCTTTTCTCACCAGGGTAAGAAATGCAGGTATTTGCAGAGGGGAGTGAGT
030	197	197 A G	:	TGGGCAGAGCACAGGGCAAGGACTTAAGGGAACTTGTGGGGGGAAGAG

				CAACAGGCTCATGGAACAGAGCCTAGGGATCCAGGAGCATAGGAGGTGGTGGTGGTGGTGGTGGCTGGGCAGGGCTC
	_			TGCATCCCCTTTCCTCAGCACAGCACCATCTTCACCCTCCTGGGAAAGCAGCATTGGAGCCTACACC
WI- 21703c	134 A G		!	AGICTTGTGCTTTTCTCACCAGGGTAAGAAATGCAGGTATTTGCAGAGGGGAGTGAGT
				COCTTGTCAGTCTGTCGCTCCACTGCACTGGCGAGGTGAGCCGGCGCGCTCATCTTATTC
WI- 22683c	139 GA	- -		CCAGTCTCGGTGAACATGGGCTCAGTCTCCCCGGCTCAGTGTTGGGTTTGCACTGGTGCACTTACAG GC(GA)GAAGAGGCTTCCTCATTTGCTGAGGGCTTTTCCTGAATCCGTGTTGAATGTGGGT
			٠.	CCCTTGTCAGTCTGTGCCTCGCACTGCCGAGGTGAGCCGGCGCTCTTGATCTTA
₹	-		•	TTCCCAGTCTCGGTGAACATGGGCTCAGTCTCTCCCGGCTCAGTGTTGGGTTTGCACTGGTGCACTTAC
22663b	55 C T	T		AGGCGGAAGAGCTTCCTCATTTGCTGAGGCTTTTCCTGAATCCGTGTTGAATGTGGGT
			_	OCCTTGTCAGTCTGTGCCTCGCCTCTCACTGCGCTGAGCTGAGCCGGCGCTCGCT
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22631a	52 T	c	i	TATGTACCATCATAGGGTACTTGGACAAATCAACTGAAATTTTT
				AATCCACACITTCACGGAGGGGGGACCAGCCTGCCATGTCGTCCCACAGGCTCACAGCAGCGGCGGCTAC
				TCTGCTGGTGGTTTGGTGGCAGGTGGAGGTGGTGACGGCGCATTGGAAACCGTAAGGCATGACAACG
				GGAGGCCCGCGGGGTTTCAGGTTCGCGTTGACGCAGGTGCATGGCTGGC
WI-20258	157 GT		•	AGGAGGGAGCGCAATTCACAGCCTCTTGACGTAGTTTCCGGGGAAAGTACC
				ACTACACATATGCTGATTTTCAACAGTAAAAATAACATTTTACATTTGTAGAGAAAATCTAGGGTCT
			···	ACTAAATAATCTAGTACTTGTTTCCACTCTCCTGCTAACTCTGACAGGAGTGTTGTGGGAAACGAAGT
	_			CTGAAAAGGATTCAAAGGGGGCTAGGATTTGCCACAGATCCTGTAAAGGAAAGGATGAGGTGAGCTT
WI-22714 212 CA	212 C			ACCAACCCCACATGAGGGGCCAAACATCCTTAACAAGCTAGTTGCT
				TGGGGCTACTTTAGATGGGATGGCGTCAGGGTCTGGGAAGGCCTJGAJTCTTAGAAGACATTACCCA
				AATGATGAGGAGGCAGCCAGTCGTCGAAGCCATAGTTTGGATGGCGAGACTTTTCCGGCAGAGGAAAT
ķ				AGCAAGTGCAAAGGGCCTGAGGGAAAATGAACTTGGGCTTGTCCTACAGGGTGAAAGGCGGCCGGT
22734a	44 GA	Α'	_:	NTGGCTGAGGTTTAGTGGATG

				TGATATGATGTCTGAGATTTGCTTCCAAATATGCCTAGGAAGGGAAGAGAGGAGTG111AGAGALALAGAA CAAATCAAGGTTGTCAAAATGTATAGTAACTGTTAAAGCTTGCTAAGGGT(A/GJGTTATTCTATTT
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				TGCTGTTTCTTTAGTTCATGACGTTTATCACAATGTGCTACTGTTTCCATTGATTACATGAGGAAAAATAAAT
× t				TATTIGITIGAGCACAGGGCCAGATGGGAACTGAGGTATGTAGGTGTTGGGAGCCAGGAAAGGAAG
22775a	60 A G			931
		-		CTTTAGCTAATGAAACTGGCTATGTGGACTATGATAGACCAAGAAAGGTACCCAAGTCCTGAGGGAG CCTAATCTCTGAAATGCAGAAAGTACCCATGACAAGGGCTACAGCTTGGCTTTAGCAACCAGGA
				GGATGAAGACTJAGCAAACTGATTAAGAGAGTAGGTATAAGAACCAGGGAGAGTGGGGTCCAAAT
WI-22808 143 CT	143 CT			ATC
				TCTCTCGTGTGTTGAGCCCTCATCCCCCTCCAAGCCCTCATGCCACCACCACCACCACCACCACCACCACCATTCCAACCTCAAGCCCAACCTTTCTGAAGTCCAAGCCCAAGCCAGAGCCCTGGCAGCTTTTCTG
				GGAGACAGCATGAAAAAGGAGGGGAGTGGAATGGCAGAGATGAGGTTGAGCTGAGCTGTGGGGTC
WI-21016 207 GA	207 G		:	CTGAITGGCGTGGTGGTGGGGGGCCCAATCCTGAAGCCTGAAGCTTCA
WI-21031			1	TTGAACACCTGACCTGTGACATGTGGCTTCTGGTCCCATTTGTCTCCACAGTTGCTCCTCACAGGCAGCAGAAAACACACAC
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				GATTCAGTAGGCCTGAGGTGGGGCTTAG(GAJAA AGIA UGAMAACCTICCTACTATGTTCTAAAATGTTCTCTCCTTCTTTAAA
WI-21186	95 Q	- 		GGAGAGACAGGAATTCCAGAGAAACTGCTAATTTAAGCATAATGTATTGAAT
	1			CCACGATAACTATAAAAGCAGAAAATTAGCTTTGAAAATCAAATAACATATTTAGTAACACACATT
				CATTITIATAAACACACATAAAGACACCQAGIGGNTCTCAGTAATGCTCTGGIGCAGGGGIICICAA
.i.				AGTATGGCTTCAGACAAGCCCCATTTGACAACACTAAGAACAAACA
21187a	94 A G	G	:	CTACCTACTGATCTGAATCAGAAACTCTGAGGGTGAGAACAAACA

0016			i	THTCCCCACATACCAATGCACCTGTHGTATAAACTATH/C)GTGGGGTAAGCCCTTCTTGGAGAC CAGTGACATAGAGATCCCATTATATTAAACAAATAATAATAATCTGTACTATACTGC TTTAGTTATCTAGTGATTGAGAAAGGAGAGGAG
	3			ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAAACTTGGAAGGAAAAGAAAA
WI- 19937d	186 GA	A		GTAAAGGTGTTCTATGGCAACAGTGATGACATTGGTGTGTTCCTCAGCAAGTGGAJTCCAAACCTTC CAAAAAGAAGCAGTCATTGAAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
				ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAAACTTGGAAGAAA GAACTTTATAGACAAGCAAACCAAAAGATGTATTTAGACAAGCAAAGCACATGTTGTACATTTAGACAAGCAAAGCATTGTAGTATTTAGACAAGCAAAGCATTGTAGTATTTAGACAAGCAAAGCATTGTAGTATTTAGACAAGCAAAGCACTTCATGTTGTCT
WI- 19937c	185 C T	<u></u> -		GTAAAAGGTGTTCTATGGCAACAGTGATGACATTGGTGTGTTCCTCAGCAAGT[CT]GTCCAAACCTTC CAAAAAGAAGCAGTCATTGAAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
				GAAAACGGGGTGCTAAACAAAGAAAGTCTCAGATCCCACTGAAAATCTGTTCAGTTTCACGGCTC
WF-	227 CT	<u>;</u>		TCCCAGAAAAATIGCA ATBIACCAATI TGCATGTACCAATTTCCTACAGTTCTGAAGAATTAGCAGT TCCAATTCTACATTCTACAGTTCCTAGCTCCCAATATTCCTACAGTTCTGAAGAATTTAGCAGT CCTCTCATTTCTACAGTCTGTATTTGCTTTTCTACTGAATCTTGGGTGGG
				TCACTTTTGATCATAATCCCCTGTAAAAGCTAAAGTTATTCACATATTACAGGAAGAACTCTGTTTTCCT
¥			_	AAACAATACTGGAATTCACATTACAGACGACGAACCAACATGGGATGCCACACATAACTTCCT
21122a	42 CT	T	:	TTGTAGGTTTCACAGAGCCTATTTGTGGGTTGCT
WI-01054	5.3.A	5314 6		CAGTTTTGGTACAGGAAGGGCCCATGAATGTGGGCGGAACTATTCCACAGGAG(AYG)CAAGGAGAAG CTGTTCTCTGG
WI.21054	1986	-		AAGGAAACTGCATGGGTACAAATJGTJTCCAATTCATACTTAACAAGGTGGGGAAACGGGTCATTCT TGGCCTGCTCCAGAACAAGGGGCGAGTCTATGCACTCGTG
				GGGACCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATTCTTTCCCACTGAGCCTGGCTGAAACTACCAGCTTGCCATTTTCCCAGCTTCGTCACTCTAATTTCAAGCTGAAA
WF 21059b	181 T C	 	:	AATCCTGGGGAAGAGACATACTTCACTGAAGTCATTCTCTATTQT/CJATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCTAAT
				GGGACCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATTCTTTCCCACTGAGCCTGG[C/T]T
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- 07770	27 T	<u>.</u>		CA
M1-20442	+			GTGACAAGAGGTGAAGCAAGGGACAAGGGGCAGCAGGGCAGTGT/CJCTCGGGGCCAATGTTCAAGA
14/1 04 02E	13 T	:	ı	CAAGCTACGTA
CC212-IM	2			ATCAGAACTGCAATCTGCACATGAAAAGACCTGGGGGGAATGCCTACATCTGGAATTTTTCACAATTCAAATCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATTCAAATT
				ATCAACGTTAAATTTTGTCCGACCAGTTCTTCATTGCTGATCACTTTTAACGAACTTCAAAGG
×				GAAACTCCTGAAGCAAATGAATATTTACCTTGTGCTI ICAIGCAAATITTCT
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				AITAATAATTACTTCAGAGTAAATGCGATGICCIICACCICAAGCAIIIAICAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGAATTAGA
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			-	AAGAGCTGGTGCCTGCTGGAGGCAACGTCCAGGTCCGGGAAAGGCACIUGIGGTGTCTGTAATATCCTGTAA
				TCAGTGATGGGAGGTCTCCACTCGCCCCACAGGCAGGCTCGGGGGCCAGAGATGATGCTGTCC
	7			TCCAGTACAGGGGCTGCGTCGTGGGGTCCCCAACAGCTCCTTCTTTGGGGG
71C17-IM	5			CACATAGTTTCTCAAGAAGAGGATGAACTGAAAACTCCTCTAAGGCAGGACAAGGAACTTCTCAAGGCAAGGAACTTCTCAAGGAAGG
				ATTCTTAGTTTAGACCAGAATCTTTAATTTTATATTCTCCTTTAAIAACIGICAAAAIAAACAAAAAAAAAA
				CTTAGAGGAAAATATTCACAGTATACCAAAACATTTTAAGATAAAGAGGCAGIGIAAAAAAAAAA
₹				TATTCTCTACATACCACAGTATACAATGATGCCTTCCTGCAGGIIIAGGAAC
21513b	1921G AI	Al		

				TIGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTTGTAGGACTGGTCATGAGGTGATGCGATGAGGAGGCAATGCGATGACGATGACGATGAGGAGGCAATGACATGAGGAGGAGAAGAAGTAACATGAAAATTAAAAATTAAAAATAAAAATAAAAATAAAAATAAAA
				TJACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAAATCTCCTTAGCAAAGCTTAGGAACT
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\$,		GCCACAGGACTCCAAAGGACTCAGAAAGCATTTACAAAAGGTCATAAGGAACT
14a	100 A G			ANTITAAGGCICAGATIGGGGT TAAGAGGTGATGAATGAATGAATGAATGATGATGATGAATAAGCCAGACAAAAAAAA
				ATCCAATGTATCATTCTACCTGTATGAGGGTACTT
WI-22020	5 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	::		TICATOGGITOTTAATACAGTACAATOCTTTTGTTGAACAAAAGTCACACTGGCAATGATTACA
				GATCCAAAATAGACTCAGGCTTCAGACATAAAAAATTTAACATAGAAAACTACAGGTTCTCTCCACGGGGA
-iw	_			CACAGAANTTAAACATCIGCCCAGAIGIACACAAIIIGGIAGAAA
19576a	113A	A G		G CAN TO TO TO TO TO TO TO TO TO TO TO TO TO
				ATACACAGGCCACAATTGCAGGATGGAAAGGCAGTGGGCATATGTAGTAGTGGCCAGACCTTTCAA
				AGCAGCCTATCTTTACCAACCAGAAGIIICIIGGGGCCACAGGCCACAGGCCACAGGCCACAAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCCACAGGCACAGGCACAGGCACAGGCACAGGCACAGGCACAGGCACAGGCACAGGCACAGGCCACAGGCACAGGCACAGGCACAGAGCACAGAGAACAAC
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95a	141 A			AGTGGGAGGAAATGTGATTACTACTACTACTACTACTACTACTACTACTACTACTA
				AAACCCAGAATTTTAGGTACTTTTGTATTATGAGGAACTCACTGACAGGTCTCCAGTGACAGGGC
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¥				TCATCACCTAAAGIGAGAGGCIGICIAIICICAIICICAIICAGGCAGG
21574a	235 CT	L	:	GGGGAGGAGGAAGGAAAGTAAAGTAAGAGGAAGTCTTGAGGAAGTCTTGGGGT
				TGACTGCCAAGATTTAGGCCCCAACTTAGGAGCAAGGGICACCICIAACATAGTTAACAGACTCAAAGTGTACATACAAGCTTG
	_			GTGACCCACTGCATAAATGGATTTCAAATCCATGAATGATGATGATGATGATGATGTTTAACATGTGTTCTCAGC
×			_	TTTCATAAATAAGGAAATITCTTTCTAAATATGGCAACAGCACAGGCACAGTC
216440	151	V	:	TOTOTITAACCICCAAAAGICCCAAATAAACATATAGACATTITGANTATAGCTATCIG/A/JITTTAACA
				AACCTCATTATGATCACTGTTGCAATTTCAGTCACCTAAAATACGGAACCATGACTATAATAAACA
			-	TTTACTGTGTGGGGTTTGTTGGGACTGAACATTAACCATACGTGTATTICIAAGGTACTAGGAAGT
Ż			-	GGAACAGCTACTACGGGTCAATGGTATTTTGGGCAGTTGGCTGTGTGTG
216140	S S			GACCGAGAAAAACTGCAAGGCATATGATGTTTGTCGAAGTATCACATGACTATTTCAAGCTTATAGA
			-	GAAACTTGCAAAAAGTACAAAGATGGCTATTTTAAATTTCATACATA
				CTTTCACTGAGTATTATICTJAGGACACAATCGAGGAIGIAAICIAIIIGAAIIIANACAAAAAAAAAAAA
21615b	151 CT	CT	-:	TATTCTATATTGGGCCAAAGGGAAAAGGTAGGAAGGAAGG

				TGTCATCTCATTCTGGAGAATCATAGATGTGGCAGAAATACATATTCTTGAAGAAAAAAATTAJGT CTCCCTTATGGGTACTGTGATTTCAATAGGGTGTGGGATAAGTACATGAACAACATGCATG
WI-21981	P = 0			TOCCAACTAGCCCTCTCCAGTATTTAGATGAGGATAGAACAGATACGGTGTAACACGCCTCTCCACTGCTTTTTCAGTACTGTGTGTACCAAGAAAGCAGACTCTCACCAACCTGGCCCCTTTTTCAGTACTGTGTGTACCAAGAAAGCAGACTCACCAAGCCAACCTAACCTGGCCCTTTTTCAGTACCTGTGTACCAAGAAAACAGAAAACAAGCTCACCAAACAAA
W. 21660 120 CT	000		1	GCTTCTCAGGATGCCCACACACATACTGGGAACTGGGATGCAGGGAGAGCCAGGGTCGTGTCTTCAGGAGGGTCACAGG
20017-14				TGGAAAGTAGCCCTTCTGGACAGAATATTGTGGTCCATGTGGTTTGAGTCGTGTGTGT
WI- 19105c	211 CT	···	1	GTCTGTAGGTTTCCAGGGCTGGGCACAGAGGTGACAGAGGTGCCCAGGGTGCCCAGGGTGCCCAGGGTGCCCAGGGTGCCCAGGGTGCCCAGGGTGCCCAGGGTGCCCAGGGTGCCCAGGGTGCCCAGGGTGCCCAGGGTGCCCAGGGTGCCCAGGGTGCCCAGGGTGCCCAGGGTGCCCAGGGTGCCCAGGGTGCCCAGGGTGCCCAGGGTGCCCAGGGTGCCAGGGTGCCAGGGTCCCAGGGTCCCAGGGTCCCAGGGTCCCAGGGTCCCAGGGTCCCAGGGTCCCAGGGTCCCAGGGTCCCAGGGTCCCAGGGTCCCAGGGTCCCAGGGTCCCAGGGTCCCAGGGTCCCAGGGTCCCAGGGTCCCAGGGTCCCAGGGTCCAGGTCCAGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCAGGGTCCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAGGGTCAG
				TGGAAAGTAGCCCTTCTGGACAGAAAGAAIIIIICUJIGGGTCATGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
WI-	-			CTTGTCTGTAGGTTTCCAGGGCTGGGCACAGAGGTGAGGGCAGAAIN I GASSSSICCAANT COCCACAACTTCCTCCAGGGCAGGATTTCCACCAGGGCCCAGGGTGCCCG
W-	2			CAAACCTAGTCACTCTACTGATGCAAATGATTTGGAGGTGTTTCCTAGCTTTCCTAGCTTTACAATAAAAAGGACGGAACCTGAGTGCAAATGATTTCAGGGCA
21760c WF	8			CAAACCTAGTCACTCTACTGATGCAAATGATTTGGAAGGGTGTCTTCCTAGCTTTACAATAAGNGG
21760a	35 4	35 A G	1	TCTGCCATATTGTTCCCAGCACCACTATTACTGTTATTATTTCTCTTTGAGGAAAACCAAAAAAGGA
\$				AAATCTGGTTTGAATTTCCATGATGCCTAACTCTATGGTTAAAAATUUTTTACTCTAACTVCTAATCTTTATCTCTAACTACTACTACTACTTGCGGGGGCC
21569b	198 T C			CCAACATGCAACATGCATCTTCATTCTTAAAAAGTACATAGTAAAGGGTATGAAAAACATTGTATTCA
₹				GAGAATI/GITCTAAGACAAATGGTCAAATATTCAAATGGCCTGGCACTAGTGGTAATTCCAGGAGACAGAC
20934a	72	72 T G		AAGOCCI I I I I ACCITICATA I ACAATA ATAATA TOTA TOTA TOTA AAAA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA ACAATA AC
				TTTCCATTTATTCAGCCGGGACCATCAGAACAGTTCCTCAGAATGGTGGGATCTCAGACTTCTCCCAGGCAAAGGTAAAGAAAG
WI-21561		55 T G		AATAATTTTGTGTAATCTGTTTAAAAAGATTTTTGGATGCATTGTCCCC

WI-	1			AGCTITIGCITGAAAATITIGGTACTTACTACCTITIGCAAITCTCTITATITATTATTATTATTATTATTATTATTATTATTATT
				AGCTITGCTTGAAAATTTGGTACTTACTACCTTTGCAATTCTCTTTATTATTATTATTATTATTTTTTTT
21961b	7 C			CCCACTTGGGTCTTTTCAAGTGAAT[T/G]TTCCTTTCGTTCCTGTTCTAAAGCCTTTTAAAATGAACTTCCACTTGGGTCTCTTTAAAATGAACTTCGTTCTTTCGTTCCTGTTCTTTCT
WI-21356 251 W	148 G	; ; ;		CAAACATACATTATGGCTGCCTTTATTAAGAAATGTTTACTGAGAATCTGTACTGTAACAACATAT TTTTGTTAGAAGCATGAGTGAGTGTGTGTGTGTGTGGCGCGCGC
WI- 21930c	146 GC		;	TATACTGGTTTTTGGTTACATGGATGAATTGTCTAATGGTGAAGTCTGAGATTTTAGTGTACCCATCA CCTGAGTAGTGTACATTGTACCCAACTTGTAGGCTTTTATCCCTTACCCTACCTTCCACCCTCCCAT TTTGAGTCTGCCATAGTCCATTATATCACTCTGTATGCCTTTGCATACCCATAGCTTAACTCCC
WI- 211398	1651	0		GCTCTAGTGAAGAAATTCAGGACGGTCTTCAGAGCAGAG
WI- 20317b	217 GT	T.	:	CACTGCATGGAAATACACAGGTAACATTTTTAAACAGTGGGGACAAAATTTAAGTACGTGGGCAAAA TGTTGGTTGTTGTGGGTCATTAAAGACAATGTTAAGANTCAGGAGTACTTAAGTGGTGGTTACA AATTTTGTTCTTCAGTTTTTCATTAAGTAAATTCTAATAGATGATAACATATTACTGCAGATAAA ACCATCATCAGAAA(G/TJTATAAATTAATTGCATATTTTGAGGCTACTCT
WI-	179 GA		:	CAGGACTTGGTTTGCTGTCCCAACTGCACATAAATGTCCCTTTTTGTTTG

	Α	166 GA	21079c
CLCAGGCACCCTACACATCTGCCAGGGTAATAGGCATGGGCAAAT			<u>*</u>
TTTAATACCAGTGTGCAGCTTTGATTACTCCCCATATTACAACCCACTGACCATCTCAGCTCAAA			-4:
AATGAAAATGCCACCCAGAGGTTAACAGCTTGCCATGCATG			
ATGGTA		138 C.G	21761b
CTICIGICAATACACACAAAGCCAAGCGTAACTTGGCTGCCTCAGGAAGGCTGGCAAAGGCTGGCT			Į.
TITCTCTTTGTGTACAAAGGATTCAAAATATTTTCACATCTTCCTTC			
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GATTCTCTTAAAGAACACATACACACATGTGCACACACAC			
TGACAGATCACACCACATTITGTTTGTAACTTTTTCTCCTTCAAGAGTCACCTIAGCLIAAGACAGATCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA		L_	27
ATACTAACCCATTGAAGGATAACTATGGAAACCTTTAAATGGGAACAGTGGG	:	S 1 66 C	WI.22132
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CAACOTTTAATCTGACTTGCCTTTTACTATCCTT[T/G]CCCCATTTCTAATCTCTTTTTGCCTTACAA		_	
AII		82 GA	21723a
GCAIGAIAAAIAAIICAACIAIGAA			<u>*</u>
TGGACTTTAAAGCTCGGAJACATAAAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC			
AAGCGATTTTATTAAATTGATTGGACATACTGTAGGICAAATAATTGCCCAACAACA			
ATT		125 A G	21723b
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TAAAACAGTGTAGTTTGGTACAATAACACATATAGCAATGATACAAAI IAGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAA			
AACACAAACTCCATGCTTTCAAGATTCCCACACCCAGATACTAAGACATATTACAGCAAT		5	220022
CTCCCCCACAGGAGCCCACGATTCCAAATCCTCTTTGCTGCAACCTCT		10,73	W-
AGGGTACACGGGGGGTCCGGTTCCCGCCGAAGGACGTATTCGCTGAACTGGGAACAACAACGAACG	_		_ :
MIGHTHTCCTTTTTGCATAAGAAATATGTCCATTTAGTCCAGAGGCTCTTGCTTTATCCGGATGACGG	-		
CAGGACTTGGTTTGCTGTCCCAACTGCACATGTCCCTTTTTTGTTTG			

	F			AATGAAAATGCCACCCAGAGGTTAACAGCTTGCCATGCATG
				TGTTTTAATACCAGTGGCAGCTTTGATTCCTCCATGAAATTAAAGCTGTGTTGTTGTTACA
-tw				TAACTCAGGCCACCCTGAAATATCTGCTAGTGGGGAATTTACAACCCACTGACCATCLCAGGTGACTCAGGTGAGGGAATTTACAACTACAAATTGGCCAGGGAATTTAGGAGGAAATTAACAAATTGGCCAGGGGAATTAAAAAAATGGCCAAAAT
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Š				AATGITTAGCAATCTCTACTACATTTCAAATATAATAATTTGGTTGCAAATTCCAGNAAAGGGCA
22129a	45 T	:::9	•	TTAACCAAACATGGGACTGCTGGGGGCTTCCACCTGACTAAGGTTTA
				TGGAGTTAAGTGGGGCTCTGCTATTTCCCCCAAGAAGGACTCGGAAGATGTTGATTCCAGGGCAGAGT
				GAGGGGCAGACIAGIGGATGAGGCTCTTCTGTAAAGTCCAACAGACGCTCACAGATGCTGGGAGGCT
_				GGGGACTGCCAGGTTGGGAGCCTCACCCAGAGAGCTCACTGCATTGACCCCACACCCCACCACTCACC
14/1.21041	79 4 5	:	;	CAGCACACAGGCACACGCCACACACACACACACTGCACTCACCACGC
1017	?			AATGGCATCCCTGTCGATACCAAACATCTTCAGCAGCTCAGCCTGGCTTCCCACTTCTTGGTACCC
				GETTAACTGOCAGGINGGGTGACAGTGATGCCAGGGCTOGOCCACTACTGCACTGGACACAGCCTCACC
18016h	42 C T	!	:	AATGCCACCTTCATA
	:			AATGGCATCCCTGTCGATACCAAACATCTTCAGCAQACCTCAGCCGGCTTCCCACTTCTTGGTACCC
148				GGTTAACTGCCAGGNGGGTGACAGTGATGCCAGGGCTCGCCCACTACTGCACTGGACACAGGACAAAAGCCTCACA
180162	35		:	AATGCCACCTTCATA
50.00	3			TTCCCTTCTCCCAAGAAGTGGGCAGAAAAGCTTTGTTAACCTCCTTTTACAGATGAAGAAAACAA
				GATCAGAGGTGCTAAGTGCCTATAGCCTAGTGCCAGGNCTTCTGGCCCAATTCTGGGTTCTCTGGGCTTCTGGCCTAATG
Š	-			CCCATGCTTCTTCCACAATCTTTACTTCTTCCTCTGACCTCACCACCACCACCACCACCACCACCACCACCACCAC
1982Rc	200 A G			CTTTTAATTCTGGAAAAGAAACCCAGCTGCACACTGGGCACACTTGAACT
200				CACAAGAGTCTGTACAACCTTAGGGACACCAGCCCTGGCCCTGCCCTGCCCTAGGCTGCATGCCACCTCT
38.00				ATATCCCACCCCATCCCCAGCCTCCTGCCCCGACACCCAGGCTCCCTGCTCTGCTGGTTGTTTTTTTT
210835	AZICT		ţ	CTCCAAGGCAGGAATGAGTCCTTGATCCAACCACGGATCT
7				TTGACCTAAAGCCTAGCATAAAATTAGCTAAGTAGAATGTTTCCAAAGATGCGGCTGCATCAGTAT
				CTOCCATOCCACATAATITCTGTTTGATTTTGCCATTCACCCATAAAATGGTGGGATCTACCICCCCI
WI-19860		51 CG	:	CCTTGCAAATTTGAGCTGGNCCTCTGATCCTGTCTAAGGATCTGAAGCC
	<u> </u>			ACCCAGCTCCTCTTACCCTCTGGCTTTCAGTAGGCTTTGGCTAATGGCCANTGAAACTGCAGGGCAAG
- - - - - - - - - - -				AGGAGTGAGGGGCTJTACAGCATTTATTTCCCTCTTTCACTCCCTGTTAGCTTTGGTAGTGGTAGTAGT
108801	90	80 CT	:	TICTCTACTBATAGITICCTTGCCCACAGTCGTAACTATIGC
120021	2			

					TGTTGGTCTGAGAATTCACAGCTTACTACAAGGAAGCTGAGAATTGCTTGGTGCCCCCCCC
198910	172 CG	<u>.</u>		•	GCACCTGTAGGGGTGTAGCTTCCATGGTTCTCCAAGCACGGGCTGTACATTACCCTTAGGCTGACCATTCCCATGCACGACTGCATAAACTAGAAGACGCTTGCGGGGGGGAATAAACTAGAAGACGCTTGCCTTGCAAAACTGCTTTGAGGAAATNTCCCCAGGAAGAAGAAACTGCTTTGAGGAAATNTCCCCAGGAAGAAGAAACTGCTTTGAGGAAATNTCCCCAGGAAGAAACTAGAAAGACGC
WI-	- 2	- <u>- 1</u>		}	AOCTGCTATTTCACCATACTATGGAGAATACAGCTAATGAAGTGGTGGCAGAAGCTTGGCCGTGTGA GTGCCCAGGGTAAAAGTCTCTTCTGTCCAGTCCA
	-				AGCCATACAATGCATTGCAAAGAAACAAAGAGCGGTGTACAGGAGTGGGGGACGCGTCAGTGTACAAT ACATTCATGTCCAGGATAAGGAGCAT/IGJACACCAGGATTTATACACGGTGGCAGCGGTATAGGCA
WI- 20270b	116	<u>5</u>		1	CGATGATACAAAATATAAAGTATATTCCATCTATATAAATACAACATGGGGGGGG
					AGCCATACAATGCATTGCAAAGAAACAAAGCAGCTGTACAGGAGTGGGGGGGG
WI-		- V	•	1	GGGTGATCTTGTTTCCCCCCCCAGGGGCCTGGGGGCCAGGGANGGGTGGTGGGAA
					CCACTTTCAATATTTTACAAAATGCTCACGCAGCAAATATGAAAAGCTTCAACACTTTCCTTTTCAACATTTGATTGA
WI-20622 130 T C	130	<u> </u>	:		TACTAATTITCINTAACITTATTITACAATAAGCCAACATCTGTCATGCAG
					TTCCCACTCAAAACTCCCACCCACCTTCCTGCAAGGCAGGGCTAACAGGACCTCCTGCCTG
WI-	190		:		CAGGAGAGGTCTATTTCTGGGGCACCCAGAAGNTCAGACACATACIGCIGGGAGACTLAGGCGCCTCATTCCCTTCTTTTGGCTCCCTCATTCCTTCTATGGCTTTAGCTGCCCTCATTCC
					TTCCCACTCAAAACTCCCACCCCAACCTTOCTGGAAGGCAGGGCTAACAGGACCTCCTGCCTGCCTGCCT
20768a	71	당		:	GTAATTCGCCTTGGTCCAACTCCTTCTATGGGGTTTCTCTCAACTCTAACGGCAA
					TGTTTGCTTTGTGCCAGGTACTCTACTGCTTTTACATAAATAA
WI-21909 153 AT	153	H			GACACTAAAGTAATATAGGATACCACTAAATTTATATTTCTATGTATG

					TGTTGCTTTGGTTGTTTGCTTTCTGGAACATATTGGAACACTTGTTTTCATAAGCTGTCCTGACAGT GGCACAATCCCATCCTCTCAGGCCTTTTAATAAGGTCATTATGAAATCTGAATTTCTJAGTTAAT
					ACTICTEGEGATTCATTTCATCTGCAAAAGCAACTGGCACACCACTOCTTGCCGGTGCAGCTCTGG
WI-22202 128 A G	128/	গ্ৰ	•	:	CCAAGGATGAAATTTCCACATTTATTTTNCTTTTATGTGAATAGAAAATGGCAGTGAAGTGCCTATG
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WI-22109	1	-			GARGAGGCATCATAGAAAAAAACCTCAGCCAGAAGTTAGGACATTGTGATTCTCAGCCACTAACGA
					GCTGTATGACCTTGGTCACTAGGCCTCTGCAGGCTCTGGTTGTTCATTTGCAAATAAAGCCA
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					GACGTCATCTCTGAGGGCTCTGCCAGGTGGATTAGGTGAAGAGGTT11A1GGGGGACTTGCTTTT
		_			GCCAGTAGTGGGGAATGCCACATGCAATGGGTGAATGTGGAAATCTGTGTGTTTAATTTGTTTCTTTATTCCTTTTATTCCTTTTATTCCTTTTATTCCTTTTATTCCTTTTATTCCTTTTATTCCTTTTATTCCTTTTATTCCTTTTATTCCTTTTATTCCTTTTATTCCTTTTATTCCTTTTATTCCTTTTATTCCTTTTATTCCTTTTATTCCTTTTATTCCTTTTTATTCCTTTTTATTCCTTTTTATTCCTTTTTT
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		_			ACCITISCACACAAAATGGGCAGCTGGGGCTAAGGCATTTAAACAAAGGCTCCAAAGGACCCTT
					TCACTTGGGTCTAGCATCCAGCCTCTCTCTGGCAAAGGCAGGATTGTGGGTCTJCCTTGTGTTTTCTG
WI-22387 186 CT	186	-5		1	AACAGGGCCCAGGCAAGGCATGCCATCACTGCAGCACTCAACC
		1			GCCGTTCCAGTATTGATAATTGTGTTTAATTTCTATACAGAAATGGTTCTTICTIGAAIAIIII
		_			GTAGGGATGGATGAATTGAAAGTGAATTAAAGTCAAGAGGGGGGGG
W					GAAATGTTACCAAATCCATAGTGAAGAGTAGAATATGTTOTTTAGAAGTGTTACCAAATCCAAATGTTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTGTAGAAGTAGAAGTGTAGAAGTAGAAGTGTAGAAGTGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGA
22395b	127 A G-	<u>¥</u>	1	•	CTOCT
	_				TTTATGGCTCCTGAGTGCCTTCACCCAGCTACACTTTACCTIGIALCIAAAAGIGIAATTTAATGGCTCCTGAAAACTACTGAAAAAAAAAA
		_			AAATACATTGGCTGTAAAGTCG[A/C]GATCAGGIGCICIUUAUUAAAAGUAAAAAGUAAAAGUAAAAGUAAAAGUAAAAGUAAAAGUAAAAGUAAAAGUAAAAGUAAAAGUAAAAGUAAAAGUAAAAGUAAAAGUAAAAGUAAAAGUAAAAGUAAAAGUAAAAGUAAAAGUAAAAGUAAAAGUAAAAGAAAAGAAAAGUAAAAGUAAAAGUAAAAGUAAAAGUAAAAGUAAAAGUAAAAGUAAAAGUAAAAGAAAAGAAAAGAAAAGAAAAAGAAAAAGAAAAAGAAAA
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					ATCTGCATGATTAAATAACATTAACAAGTAACAGTATCCCTCAAAATTGCACATTCTCCTCAGTT
, W					GITGAAAAAAAIALUUUUAAAAAAAAAAAAAAAAAAAAAAAAA
21342d	2	59 T C			

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				CATACCCTTTTAGGTGCCCACATTGATCATAGTTAACAGTCTTGTAGTTCTCTCTTGTCAGTCTTGTCAGTCTTGTCAGTCA
₩.				GCTCTCCCACAGCTGATT[A/G]CAGACATTGCCTGTGCTTCCTACCCCAGCAGCTGTCTAGTGCTAGTCTAGTCTAGTGCTTGCT
21763b 1	154 A G			(GA
				CATACCCTTITAGGTGCCCACATTGATCTTAGTTAACAGTCTTGTAGTTCCCTCTTTAGGCTTCAAGA TAATTGTGATTCATCGCACOCCAGATACTTCCAAGTGAACCAGGCCTCAAGACTGTTCAGTCAG
. ≱				TICIGETETECCACAGETGATTACAGACATTGCCTGTGCTTCCTACCCCACAGLAGETGTGTAGTGCCTGTGCTTCCTACTACAGAGAGATACTGCCTGTGCTTCCTACACAGAGAGAG
63a	135 T			GA
				CAGTCCATTIGAGTCCCCAGTCGAGGGTGCATTCTTCCTTTATCTTGCTTAAGCCACTTGAAAAAAAA
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4				TOCCAAGTOCTGATGGATTCAGGCAAGACCTTCACACATTCACCACTACCTGCTGGAGAGAGGAGAGGGAGAGGAGAGGAGAGGAGAGGAGAGGAGGAGA
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218039	-			CACCTGGCAGTTGAGTCAGATTGTAGGAAAATTAACCCAGATGGGTCTACATTTTTNTTCAAGTTCA
				AACCACATGGTTTCCTAGTCAGAAAGTCTCATGGACTTTCTTCCTAAGC/GJTGTTCTATGATCAGAC
Ž.				CACCTCCTAAATGTGGCTTTTACCCATTACAGGCTACAGTTGAATCAGGCAGG
216876	11500		1	AG
	-			AGCTITTACAACAAAGOGAGGGTTTAAGGAGCCTGAGAAGTTTTCACAACTATTGACTATTGACTATTGACTATTTTAAGAAGAATTTTAAAGAATTTAAAGAAGAATTTAAAAGAAG
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223743	149 T C	- 5		TATTCAGTAACTAAATTCAGGATCCTGCATCATTCTCTTCACA
2007				ACTTGTCTTCAGGCAGGCATTTCTGGGATCTAAACTAGAAATCCTTGAAAACAAAATAGTAGCAGCAAATAGTATATATA
3				CTTICAGGAATGTGCATTCACTGTAGTGGGTTATTATGGGGGGCTCTGCCTGTGGTGGTGTGTGT
222504	132 CT		•	GGANCCAGGAGTGGAGGAGAGGCGGAAATAGACAGGGGGAAG
2000	2			ACTTGTCTTCAGGCAGGCATTTCTGGGATCTAAACTAGAAATCCTTGAAAACAAATAGTAGCAGCA
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222500	000	:	<u>:</u>	GGANCCAGGAGTGGAGGCGGGGAAATAGACAGGGGAAG
B00222	3			GCAGCCATOCTCCTCTCCAACACCTCCCAGGCCACCTGGGGGCCAGAGCACCTCATGCCCAGCAGCAC
				CTACGTGGCCCGAGTACGGACCGGCCTGGCCCCAGGTTCTCGGGCTCTCAGGACGTCCCAGGACGTCAGGACGTCAGGACGTCAGGACGTCAGGACGTCAGAACGAAC
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04932-2h 192 GC	192	-:- -:- -:- -:-	:	TTTGACGGGGCCGCCGTGCTCAGCTGCTCCTCGGGAGGTGACGAGGGCCCGCCC

U/IR- 04932-2a 149 C/T	149		1	GCAGOCATOCTOTOCAACAOCTOCCAGGCCAOOCTGGGGGCAGAGCAOCTCATGCCAGCAGCACCCGCCAGGCACCAGGCACCAGGCACCAGGTTCAGGAGCACCAGGGACCTCTCAGGACGTTOCAGGCAAGTGGAAGCTCCCAGAGGTTTGQCTTTGGGAACTCCCAGGGGGATGAGGGCCCAGGGGACGTGCTTCCTTC
	C			GTGAGGAAGATGGACCTGGACAGTCAGCTCCACACCTTGCGCTGAGCAGCTGTGATTGTGCCAGGCGCTGAGCAGCTGTGATTGTGCCAGGCTTTTCCCAGGCCTTGCACAGGCTCTCTGCCAGGCTTCTCTGAGAGATGCAGCTCTGATTCTCCAGATGCAGCTCTGAGAGATGCAGAGATGCAGAGATGCATCTTCTGAAACATTCCAAGATGCAGCCCAGGAGAGCTTCTTGAAACATTCCAAACATGCATCAAACATCCAAAACATCCAAAACAAAACAAAACAAAACAAAACAAAAACAAAAAA
naguns	7 .			GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACTTGCGCTGAGCAGCTGTGATTGTGCCACACGGAAGAGAGACAGTTGTGCCACACACTTGCGAAGACAGTGTGATTGTGCCACACACTTGCCACGGAAGACAGTGACAGAGACACTGCCACTGCCACTGCCACGGCCCTCTCTCT
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\$\frac{1}{2}\$		C		GTCACAAGAGGCAGGGCTCTCGGGACGTCTCCACCATGGCCTGGGGCTCTGCTGCTCCTCAQTIC)CTCCCTCAGGGACTCTGGGGACCTCTGGGGTGATCGTTGGTCTTGGTCTTGGGGACCTCTGGGCTGATCGTTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCATTGATCAT
stSG1001	70 T.C			GITCAGGCTCATCTTGAACTOCTGGTGTCAAGCGATCCTCCCACCTCCGACCTCCCAGGGTGCTGGGATTATTATCTCTCAAGGATATAGGTTACTTTAAGAGGAAGGA
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91853416				TEGETTCAAGTGATCCTTCCACCTCAGCCAACTGAGTAGCTGGCCTGCAGGACAAGTCACCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCA
	43		;	CCTAAGTITIGIAGAGACAG
6				GTAAAGACAAGGTTTTGCTATGTTGACCAGGCTGGTCTTGAACTCCTTGGCTTCAAGGGACGGTACCA
				CCTTGGCCTCCCAAGTTGCTGATATTACAGGTGTGAGCCACTGCCCCCCGCCGACTTTAAACTGAAT
				GTTGAAAATCATTCTGCTCTTTGCTGGGTAACACTGA[T/A]CAAGTTGCTTAACCTTTGTGAAACCAC
ets/93424 173 T A	173	T A	:	TTICCTTATCTGTAACAAATGGACAAACAGAACTTTTCCTTTCCTCCTC
2000				GTTCATGTTAAAGATTAGGAAAGCTGTGGATGTGAGGGGTCAGGTGATGTGATGGAGGCCTCACAGA
A T B B T A	ď	T A	_:	ATGAGTGGCAGAGGGCCCQT/A/GAAATAGCTTACTCTGTTTCCTATC

stSG3463 103 CT	103/0			GATACAGAAGATAGTGTGGTATGGATGGATAGTATGAAGGACAAATAATACAAATATATTTTATTG AAATAAACAAAAATGCATACACACCTCAATGGGTCAC C/TJTGGAACAAACTTGCTTGACTATATTA CTGA
				CAAGATACTTCATTGTCTCTAAGTAGTGCGGCGCAAATATTTCTCACGAACAAGGACGATTTG
stSG3491		·		AAGA(GA)GTGGAATTACTGTGCAAGGAGTACTTTACCTCCAAATAGCCTGCAATTTAGAGTGTGAA ACAATCTTGTAATCTTTTACTGGCACCTGTGGATTTCTATTAAACTCATTTATACTATTTCTGTGATG
٩	716	71 GA	-	ACAGAWATAAGTTAAC
etSG3523	33 C T			TAGCCATCTTACTCTAGTTCTTTTGGGTTTTA[C/T]GCATATATGTGTGTACAAACACACACACACCCCCAAATTCCTCAAATGCTCTTGGCATAAGTTTTATCTCTTACTGGTCTC
				AGTACAAACACAGATTTAAAGAGCTCAGCAGTATTGACACGCTGGAAATTAATGGAGACATOCACTT
		-		ACTGGAAGTAAGGAGCTGGTAGCCTACCTACAGCTGCTACAAAAACCAAAATACAGAATGGCTTC
				TGTGATACTGGCCTTGCTGAAACGCATCTCACTGTCATTCTATTGTTATATTGTTAAAATGAGCTTG
stSG3536 213 A G	213 A	O	:-	TGCACCATTAGIA/GITCCTGCGGGTGTTCTCAGTCCTTGCCATGAAGTATG
				GAAAAAGCTTAACATACGATCCATGTGCAAACOCCAAAACAGGATCTACGAACTCTGGCATGATCCA
				CATOGOTACACATACCATGCTGGAAGTGCACATCCACAGGCACGGAJTAACATACACAGTACTGT
stSG3583 112 GA	112	A	;	CTAGTTATCAACACCTAC
				CCTAGTAACATAGTGAGACCTCGTCTCTACTAAAAATTTAAAAAATCAGGTGTGGGTGG
stSG3586				CCTGTAGTCCCTACTTGGGAGGCTGAAGTAGGAGGACTGCTTGAACCCCAGGAGATGGAGGCTACAGT
ø	60 GC	o s	1	GAGTTATGATGGCGCCATTGCACTCCAGCTTGAGACTGTTTCAAAAA
				ATATAGTGCTGGTAGCATTATAAACTCCTTTAAAAAGCAATCTGGCCATATCAAAGGCAAAAAAGT
				GTATATACCACCCTGGCACAAAAACCCCAATGA[T/O]CCTATTTCCAAGAATGTATCCAGATGAAA
stSG3589 101 T C	101 T	 		GTATCCAACAAAAAGCTATATACAC
stSG3590				GAGAGATGAGCTATTTATTCTTTTACTTAATGAAGATGTAAGAAATGATCTTCTGTTCTAAAAAAA
60	70 A T	<u>L</u>	•	AAAJATITTCTCTGATGTCTCTTGACCCTGTAGGAAACACATTCAGTTTCTACACT
				CAGTGAGACTTCTCATTTTATAGCAAATACATTTTTGCAGCTTAAATTTTCTTGAATTCATATACGCT
stSG3619		78 A C		TCTGTCATTTJACJAACAAACTTCCAGAGAAACTGGGCTCTATATATATAG
				ACATATGTAACTGCCATTAGTAGCCATATTTAGGATGAGA[T/C]GGATTGAGGGCATGAACCAAGG
				ATGCGTAATAATCATTATGAAATAATAAGTTATCTGGGGAAACGGCCATTTGTCCAACATTTACTAA
s1SG3644	40 T C	: :		GTGCCTACTA
			:	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATGATGATAACAATAATATGTCTTACT
stSG3646				GGT[G/A]ATATTAACTTTGATACTTGGTTAAGATGGTGTCTGCTAATTTTCTCCATTGTAGAGTCATT
٥	70	70 GA	:	CTICTCTTTGTA

		E			CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATGATGATAACAATAJA/GJTATGTCTT
stSG3646					ACTGGTGATATTAACTTTGATACTTGGTTAAGATGGTGTCTGCTAATTTTCTCCATTGTAGAGTCATT
۵	55	55 A G	1		стстсттвта
stSG3646					CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATG[A/TJTGATAACAATAATATGTCTT ACTGGTGATATTAACTTTGATACTTGGTTAAGATGGTGTCTGCTAATTTTCTCCATTGTAGAGTCATT
8	43	43 A T			CTICICITIGIA
stSG3693	85	85.A.C]	ATTETTTOCCTGAACATTCOCGTGGTCTCCCTCTGAAAGCCGATGACCATCCAACCCTGGACTCACCT GAAATATCCTACGAGGGJACJTCGCCCTCCGAGAGTGACGATTATTAACCACCCAACGGAAAAAGG
stSG3693	30	30 C T			ATTGITTCCCTGAACATTCCCGTGGTCTCQC/IJTCTGAAAGCCGATGACCATCCAACCTGGACTCA CCTGAAATATCCTACGAGGGATGGCCTCCGAGAGTGACGATIATTAACACCACCCGAAAAAGG
3		-			TCTTGCCCTTTGTGTTACCCCTAGAGAGATGGCACACAATCCCCAGGGTTGCTCTGACTTCCACCTT
stSG3698	145	45			TCACTGACTTTTIATTGCCACACCTCCCTCACAGACACACACACACACACACA
stSG3698		<u> </u>			TCTTGCCCTTTGTGTTACCCCTAGAGAGATGGCACCCAATCCCAGGGTTGCGGTCTCTGACTTCCACCCATCACTGCAGAGAGAG
ø	51	51 CG		:	AGTOTTTATTGGGGGAGAATACCCACCCACCTTCACTGCACAC
					ACCAGCCTCATGTGCAGAGGGTCTCCTGCTGGTGGATCCCCACTGGAGCCATUCCTGGGGCATULI GTCTCCCTCATGTGATGCTCAGTGCTCAGTGATGCTGAAGGCTAAATGAATG
stSG3724 107 CT	2	ઇ	:	:	GIGGCIAIGCIGGCIACI
		_ (GCCAAAACAAAAAGATCTTTGGAGTTTACTGACGGCAGCAGTI AAI ALGACACAT LAACATCAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
StSG3/20 104 GA	2	主			CONTRACTOR OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF
_					GGGAAGAAGAAAGAAAGAAAGCAGGCTGGAGGGGAAAGAAGGAGGGGAAAGAAGGAAG
stSG3751 128 GA	128	ले	Α'		GCTGACTCCATGTTGCAAGAG
		1			TTCTGTGCAAAAGAATCCACATCATTGTTTGGTAGCAGAGGATCTCTTAT/AJAAAGTTCCCTAAGA
81203/8/		-			GACAAGAGGGAAGAGATGCGCCAGAGACCAGGGCTGGGGCAGCTGGGGGTCCCTGAGTGCCAGGGGC
stSG3880		(CACCACACGTCCTGTGGGTCAAGGCCCCTCTCTGGGGAAGCAAGTCTAAGAGGACCGAAAGAAGGAAG
٥	-	5	3		

stSG3880					GACAAGAGGGAAGAGAGACGAGAGCCAGGGCTGGGCGGCGGCGGGGGGTCCCTGGGGGTCCTGAGGGCACGGGGACGGGGACGGGAGGACGAGGAAGGGAAGGGAAGGGAAGGGAAGGGAAGGAAGAA
83	36 GC	ပ္ပ		:	GECTGGGAGGGGACCCCACTOGGGGACCCAAAAGGAGTCCATTTCTGCCCT
					AATCAGCCATTGTACACATTGCAGCTATGTAGTGTTGTTAGTGTTGTTAGTTTTTTTT
stSG3895	4 4 A	<u>0</u>	i	i	TACATGOCCICATAGATATATTCAALTAGTGTTATCACCATGGGAACAAGATGCTGATTCGTTCAACTG AAAAT
					TOTGTTGAGACTGGAGACCAGGTACCAAGCACCGACTCTGGTGGGAAACCTGGCTTCCTGATAACA
					TCATCTATTTCACCTAAATGTGAACTGCTTTCTTTC[T/CJTCAGCTCAATAGCTTAACATCTAATTC
stSG3902 104 T	104	O	•••		ATGITTGCTCCCTTTGCTGGACAAT
			-	-	GGGTGTCTGACGGACAGGCACACCCAGCAGTTTCAACAAGCAATTTGTCCGGAJCTAGTGTGCAGGC
stSG3935	50 GA	<u>ح</u>	•••		TCCTCCCCCAGTTTCCCACAGGCTGAGTACTATGGGGTCACAACCTTCCTGGACGT
					GAGGAAGAGGTTGAAGAAGTGCTGA{A/GJAAATATATTTAAGATTTCCTTGGGGAGAAATCTCGTGC
					CCAAACCTGGTGATGGATCCCTTACTATTTAGAATAAGGAACAAAATAAACCCTTGTGTATGTA
stSG40	25 A G	Q			CCCAA
					GTGTGGGCTGTCTGATGATGGCGCGCTGAAGITACTCTTTACGGTCTTACACTTTTATGCTCCT
stSG4009	32 A G	B	•		ATGAATTCTCTGATGGGCTTTAAGGGCTGAACCATATCTGAAGGTTTTCCCACACTGCTTACA
					AGAAGOCTTGGGGACAATGGCAGTGCCCTTTCTGAGTAAGACATGAATGCCATCTGGAGGATCCATT
_					TGAAACTACAGTGCAGTAACCAAAGAACCTAATGTTTTCAAGCATAAAGGTACTTIT/CJTGTGAAC
stSG4033 123 T C	123	그			AGGTGGGCAACAC
stSG4038					GCTGAGAGCACGTGTACAGCCACGCCTGT[G/A]CGCAGGCCCACTCTGTGCAATAAACATGTTCTGCC
æ	29 GA	8		:	CATGITICCICAGICAGGAGGITICAGGCTCCCGGAGAGCACCTGAGGGITICCATCACT
					ACTGTGGGTTCAACAGTATTGCGTTGTCAGACTAGGAAAGCTAAACGAACAAAA[T/C]GGTTTTAGTT
					TTGCTGAAGACTGGCCTTATTAATGGACAGCTTTCCTAACAAGAGATTATTAACTTTTATCAGGTGTT
stSG406	53 T C	5	!		AACATCTGTTTCAGGAACATGGCA
		_			ATCTGGGCTGAATTAGTCAAGCAGGTCAGATACTATTGTCTGCTAGATGTATTAG(G/TJATAAAAA
stSG4095					GTTTGCTTCTGTAATACTTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGTCTTGAGAATCAAG
۵	55 GT	GT			OCTITIGACTAACCCCAGGGCATTGCCCTTCATCCTGG
					ATCTGGGCTGAATTAGTCAAGCAGGTC[A/C]GATACTATTGTCTGCTAGATGTATTAGGATAAAAAA
stSG4095					GTTTGCTTCTGTAATACTTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGTCTTGAGAATCAAG
æ	27	- V			CCTTTGGACTAACCCCAGGGCATTGCCCTTCATOCTGG
					TGCATGTTCCACATCTTTCATAACAGCAAAATGTATAAAACTTACGTACTTATGGATAATCAC(G/
stSG4120	65 GA	<u>Q</u>	;		AJCTTTTCCCCTCAGAGAGCCCACAGTTAAACACGTTCCAGCACACATTAATCCACCGAGCT

	F			CTTGGCAGATAAGGGACTCGTTTGCAGATATGACTTTCCTTTGTGTACATTTCT[A/G]TATATTT
	-			TACTTCTGAAAATGCCACATAATTTGCAATAAATGATTCACTOCTTAGCTCCAAAAGCAAGTCC
stSG4128	54 A G		1	TTTATCAAAATGCTCCAGAGGG
				CACGAAACAGATGCAGOCTACACAGTGCTGTAGGACCGAGGCTCACAAACATOCACATGGCACAAGC
stSG4209				AGGGCCGGCCACTCCAGGCAAACGAAGCCACCCCGAACCTTGCAGAGGCAAGAAGAAGAAGAAGAAAAAAAA
٩	128 GA	A		AGGGGGACCACGGAGGCCGACGGGGGCTTTGATGCCTCCGAAGACCTCACGTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTTCTTTCTTTCTTCTTCTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTCTTTCTTTCTTTCTTTCTTTCTTTT
				CACGAAACAGATGCAGCCTACACAGTGCTGTAGGACCGAGGCTCACAAACATCCACATGGAAAAA
21200			•	AICAGGGCCGCCACTCCAGGCAAACGAAGCCACCCCCGAAACTTGCAGAGGCCGCACTCCCTCGGC
81504400	A 6.0	::	_ ;	AGGGGGACCACGGACACGGTGCTTTGATGCCTCCGAAGAGCTGAGCTCCATTCCA
	3			CATTACCCAGAACGCCATGGAGGACCAGAGCGAAJCCACGGCCGGGACTCCCGCGATGGCTGGGGGG
etCG4254				GCTATGGCTCTGACAAGAGGATGAGCGAGGCCCGGGGGCTGCCTCCTCCCCCAGGGGGCAAGACGTGAA
2000	31 GA		_:	TGGGGGGACCATGGCCGAAGAGGATGACCGGTCATG
				TGCAACAGCTCTGAGAAAATCCTTGGCAGATCAAAAGAGAGGGTAGTGGCTCCCACACTTTCCAT
e15G4301	B1 T	81.T.G		TTAAGCAAATAAAIJT/GJAGCTTCTGAGTAGTTGTTCCCAGTTTCACCCAACATTTG
200				CTCACAAAGGCCAACACAGAAAAAGATACAAATACATTCATCCAGCTAATATTTAGTTTTATGACAC
				AGAGIT/GITTITCAAACAAGTTTAAGTGTCACCTGAAGAGCATGTTAAAAAAGTTTAAGTTATCACTT
St5G4331	11	ا ا		GGAGAGCAGATITCTTGGCCTCGCCCTTGTGATTCTGTTTGAGGGGTGTGC
				TTTGCAACAACATGGATGGACCTGGAGGCCATTAAGTGAAGTAATGATACAGAAAGTCAAAAACC
07675000	7.0		:	ACATGTTCTGG/AJTAAGTGGGAGATAAACAATGTGTACACCTGGACGTGGAGAGCAGAA
2000	2			TTCCCAACCATTGAGTGACAGAGCTCAGTCATGCAGAACTCAGGTTTGCATGACTCAAATTAGGCAC
#CG4361				AAGTTCTTGGAATTTTCCATAAGGGATAACTGCATCTTTTGC/A/CCTTCACAACTAGAAACGACTC
	109 AC	<u> </u>	1	AGCGACTTTTCTGTGAGCAAATGTCGAGG
				TTCCCAACCATTGAGTGACAGAGCTICICAGCTCATGCAGAACTCAGGTTTGCATGACTCAAATTAGG
e1SG4361				CACAAGTTCTTGGAATTTTCCATAAGGGATAACTGCATCTTTTGCACCTTCACAACTAGAAACGACTU
	24 T C	- 6	:	AGCGACTTTTCTGTGAGCAAATGTCGAGG
,				TTTCACTGCTACTGGTTTCGGTGTCTGAGTCCTCAAACTCTGCTTTGCAAGTGCTTCTCCAAGGGGAAG
otCG4376	73 A G		_:_	AACAGIAGICTGGAACTGCGGCTCTGCAAGAGCCATTCTTCCAAAGCCATTICTTCTAGCIUU
200	-			GAAGGCCACAAACACTCCATAGCCAGAGAATGACAACATACGATTTTCTTTT/CJTCAGTCTTGTAGT
c1SG4381		5010	1	ATCCACAGTAGTGATGTCTGTCCATGTACAAGTGTCTGTC
2	<u> </u>			ACCAATGGTTCTGCTATGTGCATCCGATATTTTTGCCCGATCTGAAATACTGCAAGGGCTTAACCAT
				TCAAACACCGG/A/GJTGACAACGAACCCAGTGGACTGTGAAACTCAGGCTGCAGGAGGGTGGCTTGT
ctSG4410		79 A G		САССТЕВЕТ

				AGCAGATCAGTCAGCCCACTTGTCTTCTCTTTTTAGGGAGAGGCTAGGCAGTGAACACATCA(C)
	_			TJGTATGCAATGAGAAAAIAACCAACIGGIAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA
stSG443	65 CT			AAATGGAATTCTATCCTGGCTGTCCTICTCAGGTC
stSG4430	F			ATGCACATTAAATGAATGGCCTAACTACTGGGAACTTTAGTAGTTCTATAAGGT[A/G]ATTAACATA
	54 A G	<u>.</u>		GGTAGGATCCAGTTCCTATGACAGGCTGCTGAAGGAACAGATATGAGGCATCAAGAGGGCATTT
	F			OCTODOTTOCOTTICOCOTTICCAGICTTTTCCATACTGTTCCCCCTCCCGCCCCACCCCA
stSG4448	99 GA	!		CGCCTAGCCCTGCCCTCGGGGTCACTGCGAJTGGGTTAGGCCCCCAAAAAA
				ATTAGCCATTCATCTTGCAACAATTGCTTTACTGTAACTAAGAGTACTGTACTGATGATGTTTACAAT
				TAACTTTGGACAACTTAAAACTTATICJTAGTGACATTGCTGTCTAATAATCAAATACTTCATCATA
e1864449	92 T C			GGCTGAACATAATTAAAAAGAGCAAAGTTACCCCTCCC
2				CAGACATGAGGGATGGCCCTGTCTCTCGGGACAGAGCCTCACAAAAATGATGTCCATGTTTTGTGT
				GAATGAAACTCCAAACACTCTTCAGTTTTTAGAGTCATTTTCTGGTATCGAGCGACCACACCGAGGAG
C1CC4467	42 C A		:	CACACCCTGCTTCCAAGGCTGCTGCTCTGCACAGT
100000	2			ACATGTCATTTCCTGACCAGG/A/CJTATTAAATAGTTTATTTAGAAGAAATGAGTTGAAGTGAGCGA
4564475	21 4 C	:	;	TTAAGAGACACAAACTGGACTTTTGTTTTCTTTTACTGTAGCACCCCAGGTTTCATG
2004	-			GTAACATTCTGGGGGGGGGGGGGGGGGACAACAAGATGAACCAATAATTACAATTATACATT
				TCAAGGAGACTTTTAATCTAGGTTAATGTGAAACGCAGCCATCAATGGTTTGTCAGGAAAAGGGAGA
c15/34477	32 A G	:	:	TGAAGTCTTGCTCTGGGGCAACGTTTGGCTTGCAGTCAGACTTGGC
2000	,			TGAACTEAGAGGTGGGGAGCTGCAGGCAGGGAGGGTGGGGGCGCCAAGATGAGCCGGCCCGGGA
				CAGCAGGCGTCCGCCTCCTGGCGTTGGTAGAAGAGGCATAGGCTGCCTTGGACTCGATCT
etSG4531	79 C		:	GATTCTCATTGACAGGGGAGACGCTGTTGTCATCAA
e18/34550		-		TGCATTAAGGAATGATACGGCATATTTGGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT
	86.6	G A		AAAAGAGACAGTGGGCACCGGAJCAATTGGAGGGGGAAGGCGGGGCAGGGTTTTAGAGAAC
012/4550				TGCATTAAGGAATGATACGGCATATTTGGGGGACAGAGAAAAGGGCTTGATGAGGACAGAGTCTATTT
6000000	RAIC	200	;	AAAAGAGACAGTGGGCACIC/GJGCAATTGGAGGGGAAGGCGGGGCAGGGTTTTAGAGAAC
5	2			AATCAGGCACAAGCTCGGGAGAGAAGCCAACAAAAGCTCTTCTGCACIA/GJATGGGAGGGAGACAC
002/200	474	: :	<u>:</u>	CATTGAAAAAGGCATCGTTCCTTCATGCAAGCGAGGCCTGGCTCCCACAGGCATGGTCTCCTTG
000000	1			AATCTGTATCACCCAGCGCTGGT/C)CAATGTACTAGTAGCTTTCCACAGGGATTTTTATACTATTC
				CTATAAGGITTTATCATGAATAAAAAGCTCACAACTCTTTTCAGCCATTGCAGATTCACATTTATCT
c1SG4623	22 T C	-		TAATATTCCTGTTCAAGATGCTCTGGAG
	1_			TAAAAAAAAACAACCCCCCCAAAAAACACCCCAGAAGTTTTGAGTTTTATGTTTTCAGATTTAAAG
				GTATITICTITCTTAGCTTCTAAATTTTGAGTCAT[A/CJATCAGAAAGTCTTCCCTACTCCAAGGTGA
etSG4843 102 A C	102	:-	;	GAAAGGA
1.) []				

				GGAATCTAAACTGGGAATGGCCGAGGAAGGGGGCTQCT/GT/GTGCACTTGCACGCCAACAACAACAAACAAAAAAAAAA
stSG4850				AGCCAGCGGTGCCTGTCGGGGGAGGTTCCAAGGTGCTCCGTGAAAAAAAA
•	38 CT		i	TIGGIGGATTCTTGGGTCCC
	F			AACTOTGAAGGGGGGTGACCTCAACCCAGCCCTTGTTTCTGTGAGGTCCTGCTTTTGCAGAATGGCCTG
				CCCCTGGGACTGGAGCAGAVGJCTTGGGTGAGCTCTAGGTGGAGGGGGGGGGGGGAAAT
e18/34879	RG A G	1	i	AAACCTTCC
2000	3			ACTGGACTGGCTCGCTTGCTGAGCCGGCTGAGCGGCGTGGGACTGCGGCTGACCACCTCGCTCTCAG
104 GABBS 104 GA	104	V		AGACTOGOCOGOCOGTGACCACGACTACGCTCTGCCJG/AJGTGGGAAAGCAGAAGCAGGACC
20040018	5			AAACAAATCAAATCCCCAGCAGTCTATGTACAGGGCCACTCCCTGCCTCTCTGCCATAGAGA
				GETTEGGGGGCAGCTGAGGAGTGGTGGGGGCTGGGCACCTTTTCTICTTCAGCCACAGGCCCCTGAGG
etSG4896 112 CT	112C	1	_:	AATTAATTGACTG
200				ACAGTGCCGATGGTTACACAATIGAJTTGTAAATGTATTTAATCCCACTTACGAATGATTAAAATGA
4664032	20,00		1	TAAATCTTATGTTTATTTCATCACTACCAAAAGGCTGTGGGTGCAGGGGTGCTGGTTTCTGGTCC
300000	-			TCATGACTCCCAGGAAAAGGTCCTJAGTTCTTAGCTTCCTCCTCCCTACTTCCTCTACATGGTCAGC
615/34950	2 4 A	24 A G	i	ACTGTAATGTAGCTAAGATATAGTAAGGCATTGCTCCCTACCCCTACACTTCAAGG
910018	-			AGATACSGGCAAAACACTGGGATGGCTTCCTGACAACTTAAGAGGTCTCCGAGTTATATTCTGGGTT
				GGGAAACACTGACCCAGCCTTATTCCTTCAAGGACTCTAGTCATTGGCAAGGAGGATTCATGAGCC
eteG4957 136 G A	136		1	CCIGAIGTGACACAGATGGGGGCCCTGCTCTATATTCAAC
20000	3			GAAGGTGCTCTGAGGAGGTGTGACTCTCCCTGGCTGACAGGGGAAGGCTTAGCAGAGCTTTGTCTTAG
1907000	10 T	<u>;</u>		AGGAGTAGATGAAAAGGAAAGTAJC/TJAGAGAGGCCATTCAGGCCAAGTCAGCAACACAGACAA
2004201	5			ACTRIGITACCTCTCAGCAGATTCAGGGGTCGTGCAGGGCTGGTTACCACAAACTCAGTAGGAGTGCAA
				GGGCTJAIGITACCCCCGGAGCTAGACAGCCTGGGTTTGAATCTCAACTTCTCCCTTTTCTTGCTGTGC
79067	7.2	7.2 A G		AACCTTG
0000000	1			CAAAGGAGAGTAGGAGCCCCAATICITTTAATGGTTTCCTCCCCTCATGCTATTTGATCCAAAAA
				CTATATACAATTTTGTAGCAGTCTCTGTATAGTTATTACACATGTTTAGAAGGGAGGG
4664007		2011	_ <u>:</u>	GGGATAGGGAGATGGTGATCCAAAAT
2000				ACAGGTTCTCACACTTTGAGCCTTTAGTGCAAAAACAJCTJTATGCCATGCGGGAAATAAAATGCTT
stSG6312	37 CT		1	ATCCAGTGGAGGCTCCCCTGATGCATTGAAATATTAGGATACTCAAGCAGAAGAC
	1			GCTCTGGTCAAGCAAATTCTCCAGGACAGAAGCAACAAGGACAGTAAACACACAC
				CAAGTGCTTTAAGATTTTAAAAATGTGATGTTTTGTCCAC(GAAJATAGTTCAGGCAA) I AAGAATAI
stSG6345				GCAACCCAGAGAATTTCTGTGAAAACATTTTGCTCTTTGGCCTGGTGTGGAAAAAAAA
_ @	107 GA	V	:	ATGGATTGAGTGATGAGCAGACATG

				TGTGAAATGTACACTCAGGTCTAACAAATACCTATTATTCTCTGGTTAAGAAGGTTTAGCAGGAGCAGA
stSG6362	88 GC		:	AT
ļ				CACATCTGTGTTTCTGGAGCAAAGGGAAACCACAGAAGGCCAGGAGTTTGGGTGTGCACTGGGTJT GTCTTTCAACTGGGTGGAACCAAACTGAGTCCTTGAAGTCTCGCTCCTGAGGCTGCAGAAGAATAGA
stSG8010	62 GT	1		TGGCTT
				AGCTCCTGACTCCCTGTTCAGTGACGTCATGTTGGTAGCCTGAAATGGACCACJGAJGTGGGAGTTAT
			٠.	TTACACCATGGAAAACTGGAAAACTCTACAAATCAATGCGTTTATTTCTTTATTTTCAGAGGGCAGGTT
stSG8022	53 GA			TATCAGCACGCTGTATCTCC
_				TGATTGTTAGGGATAAGTGGGCATTGTGTTTACAAATTACTTCCAAAGAATTCAGAAAATTGTGTGTT
stSG8032	67 GC		:	GICTIGGGAGGCAGGGTAGCAAGATAAAAAGAGGGAGGACAGCTGGGGTTGGTAAAA
etSG8064	E			AGCTGGCTCTTCCTTCTGTGCGTGTTCGGGAGGCTTCACGTCCTCQC/AJCCGTGGTCGCTGGGTGGCC
9	46 C A	:		TGCAGGACCAGGGGGGGGAAACAATGCCAGGGAGAATTCCTGTCACATCAAACAGGGAACA
etSG8064				Agc1GGCTCTTCCTTCTGTGCGTTCCGCAGGCTTCACGTCCTCGCCTGGCTGG
	23 GC		:	TGCAGGACCAGGGGGTGGGAAACAATGCCAGGGAGAATTCCTGTCACATCAAACAGGGGAACA
				CACCATCATCACCATCGAGTAGGCTGAGGAGGAGGGGGTGGGT
stSG8072	59 A G		:	AGAGGCAGAAGGAAGTCCGAGTATTAGTGGCCGCATGCAGTTCAAGCCTGTGCTGTTCAAAA
				ATACACCCACACCCCCACTCAACCTTGTATCAAATTCCA(A/G)AAGTGTAACTAAAGTATAAGAAT
				ATCATGACTAGTTAAAAGATAGCAAATACCATAAGGTACAAGTTCAAGTATTAGTATAACAAGTAT
stSGB100	40 A G			CTGAGTAACAAATGTCCTTGGAAATGGG
				AAGGCTCCTTTGAAAGCATGGTTTATTTGTTCCATTTAACTTGTTCTCAGCTATACTGAAGTATGATT
	-			GACAAATAAAACTTGCATATATTTGAGATGTACAGTGTGATGATACATGTATACAATGTGAAA
stSG8102 138 T C	138TC		:	TGATI/CJTGTCATAATCAATAATTGGTATATTGGTTTAGGAAATGTGATGGI
				CAGTGGTTCTCAAACTCCAGCGTACACGAGGATGGTCTTGTGCTTGTTAATACACAGATGACTAGGCC
				CACCTGCGGAGTTCCTGTTGGAGTCTAGGCCTGAGAATATTC(AGJTTTCTAACAAGTTCCCAGGTGA
stSG8105	110 A G	<u>:</u>	•••	OCCTGAGGCTCTTGGACTGGGAACATGCTTTGAG
stSG8130				GTGTGTACATCATTGGGAATGGAGGAAATAAATGACTGGATGGTCGCTGCTTTTTAAGTTTCAAATT
٩	96 T C	:	:	GACATTCCAGACAAGCGGTGCCTGAGCQT/CGTGCCTGTCTTCAGATCTTCACAGCACAGTTCC
stSG8130				GTGTGTACATCATTGGGAATGGAGGAAATAATGAJCGJTGGATGGTCGCTGCTTTTTAAGTTTCA
	36 C G	:	:	AATTGACATTCCAGACAAGCGGTGCCTGAGCCTGTGCTGTCTTCAGATCTTCACAGCACAGTTCC
				TTGTGGACTTCAAATTCTTTCCTTCAGATTTTAAAATGACATTATGCATGTACATATTTTAAAATTT
stSG8145				AGACACATTITAGAGAACACAATTGTGAACACAAATCTAAGAAATGAATG
P	124 T A	A	-	TCTGATTCAACACTTATCTTAAACTGACTTCTGTCAATCCTGTGTGTG

	Ì			
stSG8145				TTGTGGACTTCAAATTCTTTCCTTCAGATTTTAAAATGACATTATGCATGTACATAT I I I AAAATTTAGAGAACACAATTGTGAAQACTTACTGAAA
68	97 CT	т	•	TCTGATTCAAACACTTATCTTAAACTGACTTCTGTCAATCCTCTGTGTGAAGG
				ATTGTTCTTGCAATTGCTTGGATTTTTCAGAATAGTJAGJATAAATAACGGGAATCCTAGGGCAT
stSG8150	36 A G	:		ICGIGITHICIAIGH
<u>: </u>				AGAGGATTATGGAGAGAGAGCTGGCAGGATC(CT)CAACATTATGACCCTGAACCTCCAGAACTGGAT
stSG8340	30 CT	<u></u>		TCACTAGAAGGAGAGAGAAAAACGCTCATCAAAA
				TGTGTATTGGGTGACTGTAGCCTAAGGATAAATGAAATAAAT
				GGAGTGAACTGGGAATACTTGGTTACAAGGTATTTGCACTACCT[G/A]TGAAGCAGCACAGCATTAT
S1SG8466 1111 GA	=======================================	:: \	:	TTGAAAG
				GATCAAGCAGTGCACACGGGTCACGATGGACCAGCTCTCCACAGTGCACCATGAGATGGGCCATATA
				CAGTACTACCTGCAGTACAAGGATCTGCCGTCTCCCTGCGTCGGGGGGGCCAACCCCGGGCTTCCATGA
ESTD-ACE	:	:	:	GGCCATTGGGGACGTGCTGGGGCTCTCGGTCTCCACTCCTGAACATCTGCACAAAATCGGCCTGC
	-	Ī		ACCATCTTATACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCCTGGGATTTGAGTGGGGTC
			-	COCAGCTCCACCCAGAGGCCCCTGGGGAATTCCAGGGTCACTGTTCCTGTCCTGTGGGAAT
				CAAGOCAGCTOCAGGOCCAGAAGTGGGACTGTGAGGACATGGAGGCCTCGGCACTGAGCTGCAGAOOC
ESTD-ADA			_:	GCASACCAACTCCTGAGCTTTCTGGGCCTCTGAGTCTTGTCCTC
ESTD-AK.				GGGAGTGACAGCTAGAGCACCAAGGGGGCTCTACAGGCTGTGTTCTCATGGAGGACAGGCTTCTGCTC
168	•	!	:	ATTCTGG
	+	Т		AATCCCAGCACTTTAGGAGGCTGAGGCAEGCATATCACCAGAGGTCAGGAGTTTGAGACCAGTCTGA
				CCAACATGGTGAAACCCCATCTCTACAAAATACAAAATTAGCCAGGCATGGTGGTGGTGCTGT
		-		AATOOCAGGAGGCTGAGGCAGGAGAATOGCTTGAACCTGGGAGGCGAAGGTTGTGGTGAGCCGAGAT
ESTD-ALB	:	- 1	•	GGCACCATTGCACTCCAGCCTGGGCAACAAGAGTAAAACTCTGTCTTC
	T			TCTCCTGTCATTCCTACTCCATTAGTTCAAGGTCAGTGAAGAACTGGGGGCAATTAACCAAGTAATTCA
EST)				TGGACTGCCCAACTGCGAAACAAGAAGGCGCAGTGGAGCAGGAGTATTATGCTACGCGGTTACCTT
ENT.	<u> </u>			TTTTTATGGAGGACCGAACTGAGGCTGAGCTCAGATGATCCTGT
	-			CCAGGTGTTGTGGCACGTGCCTGTAATCCCAGCTACTCGGGAGACTGAGGCATGAGAATCTTTGAAC
ESTIP-		-		CGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGCACTGCACTCCAGCTAGGTGACAGAGCAAG
APOA2	•	!		ACTCC
				GGAAGAAAATGGAGCCTGTGGGAAGGAGGCGTCCGAGGGGTGGGCTTTGTGGCAAGCCCCTTGCTGA
				AGCAGAAGGGCGTGAAGAACCGGGAGCTCATCCACATCTCTGACTGGCTGCCAACACTCATGAAGCT
ESTO	_			GGCCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTTCGAOGTGTGGAAAACCATCAGTGAA
APSB	' :		:	GGAAGCCCATCCCCAGAATTGAGCTGCTGCATAATATTGACCCAAAC

ESTD				AGACCTCAGTITCCTCTTCTGTAAAAGGGAAGTTGTTCTTGGATCTCCATGGGGCCCAGCCAG
AT3a	:	-		GAATTCAGAGCAAAGAGACAGATATTAAGAGCTGGGGAAATGTGG
				GGCTIGCCAGGGGTTCCGTIGGGGAAGGCGGCCCTACCTGGCGCTTGGCCGGTTGCTTGGCCACCTTGGCCACCTTGGCCACCTTGGCCAACCTTGGTTGG
ESTO				GTTCGTGACTTCGCTGGCGGACCTGGTGATGGGACTCCTGGTGGTGCCCGCCGCGGCGGCCACCTT
B3AR	:	-	i	33333
				GGGCAACATAGTGAAACCCCATCTCTACAAAAATACAAAATTAGCCAGGTGTGGTAGCAAGTGC
ESTD- BA511	<u>;</u>			CTGTAGTCCCAGCTACTTGGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAAGCTGCAG TGAGCCAAGATGGTGCCACTGCA
				AGCTGGATTATAACTCCTCTTCTTTCTCTGGGGGGCGGGGGGGG
				GGCCCCCGTTGCTTTCCTCTGGGAAGGATGGCGCACGCTGGGAGAACAGGGGTACGACAACCGGGAG
ESTO				ATAGTGATGAAGTACATCCATTATAAGCTGTCGCAGAGGGGCTACGAGTGGGGATGCGGGAGATGTGG
BCL2	:		:	GCGCCGCGCCCCCCGGGGGCCCCCCCCCCCCCCCCCCCC
				CAGTGGCTGAGTGGACGATGACATTCAGAAACCCATAGAGCCCCGGAGACTCATCATCTGCGCAAGA
				GACCAAAGAGGTCAGCTTCTGTTGTCCCGGGAAAGGGAGGCAGGTGACAAGGTAACTCTGCTTCAAA
ESTO-BCA	1	:	:	ATCAACCATCCGGTGGACACTGTGGCTGCCATCTGCCTGGCACA
				AAGAAGAGAAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAAGATCTCATGTTAA
				GTGGAGAAAGGGTTTTGCAAACTGAAAGATCTGTAGAGAGTAGCAGTATTTCACTGGTACTGGTAC
ESTO				TGATTATGGCACTCAGGAAAGTATCTCGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAACAGAA
BRCA1a	-		:	CCAAATAAAT
				ACTAAATGTAAGAAAAATCTGCTAGAGGAAAACTTTGAGGAACATTCAATGTCACCTGAAAGAGAA
				ATGGGAAATGAGAACATTCCAAGTACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAAATGTT
ESTO			_	TTTAAAGAAGCCAGCTCAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTA
BRCA1 b	;	:		TTAATGAAA
				ATGCATCTCAGGTTTGTTCTGAGACACCTGATGACCTGTTAGATGATGATAAAGGAAGATAC
				TAGITITIGCTGAAAATGACATTAAGGAAAGTTCTGCTGTTTTTAGCAAAAGGGTCCAGAAAGGAGAG
ല്ല				CTTAGCAGGAGTOCTAGCCCTTTCACCCATACACATTTGGCTCAGGGTTACCGAAGAGGGGGCCAAGA
BRCA1c	;	:		AATTAGAGTCCTCAGAAGAGAACTTATCTAGTGAGGATGAAGAGCTTCCC
ESTD-C18	:		1	ACACAGGIGCTGGCACTGGGGGTCGTCCTCCTCCTCCTAATTTGCTCCGGGAAGCACATTCATCAA
		Т		COCAGICAGITIGAGGGACAGCCATGCACTGAGCCTCTGGGTAGCCTTTCAACCATGCATTCCATCTAA
ESTD-C6	<u>-</u> -	!	:	GCTCTGCAAAAT

ESTD-C7	:			ATATCGTGGCCTTAGTTACCTAGAGCTGGACAATCCTGCTGGTGGA
ESTO-	1.	ļ	·	GGCAAGTITITATIGATAGAGAGAAAICAAATAATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGGATGGACAAGACAA
ESTD-			·	TAGAACCATCAAAGAGGAATAGGCTGGTGACOOCAAAGGAAGGAGGACCTAGTAACATAGTGC TTCATTATGGTCCTTTCCCGGCCTTCTCTCACATACACAGAGGCCCTTACCAGGAACCAGAAGCCT CTCAGAGCAACCTAGCCCATTACCTCTTCCCTTTCCAGAGGACCTGAAAAACGTGTTCCCACAGAGGGCGGAGGGACCTGAAAAACGTGTTCCCACACAGAGGACCTGAAAAACGTGTTTCACAGAGGACCTGAAAAAA
ESTD-			!	ACCAGGACCAGACAGCTCTCAGAGCCAACCCTAGCCCCATTACCTCTTCCCTTTCCAGAGGAGCTGAAAAACGTGTTCCCAACAGCCGAGGTCGCTGTTTTGAGCCATCAGAAGCAGAGGAGATCTCCCACACACCCAAAAGGCCTGATTTCCCACACACA
ESTD.				GTTTCTTTCAGACTGTGGCTTCACCTCCGGTAAGTGAGTCTCTCTTTTTCTCTATCTTTCGCCGTC TCTGCTCTCGAACCAGGGCATGGAGAATCCACGGACACAGGGGGGGG
ESTD-			1	TITICIGITICCCTGAAGATTGAGCTCCCAACCCCCAAGTACGAATAGGCTAAACCAATAAAAAT TGTGTGTTGGGCCTGGTTGCATTCAGGAGTGTCTGTGGAGTTCTGCTCATCACTGACCTATCTGTGA TTTAGGGAAAGCAGCATTCCCTTGCACATCTGAAGTGACGCCCTCTTTCTCTCCCACCAATGCTGCT TTCTCCTGTTCATCCTGATGGAAGTCCTCAAACACCATTTCCATCCT
ESTD- COLZA1C			:	AGAATGTATATAGTCCTCAAACTGGCCATCTCCATTTTCAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTATGCTCTCTTTCCTGTCACTTTCAGGGTGTTCAAGGTGGAAAAGGT GAACAGGGTCCCGCTGGTCCTCCCAGGCTTCCAGGTAAGTCAACTCAAGCATATACAATACTGCCTTTG GTCAGCCTATTGAGCTGTAAATCACCATACCGTACCT
ESTD- COLZA1d			1	TGAGAGAACACCTAGTCCTCCATCTCTCTCAATGGCAAGAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGCTGGGACCTGGAACACTGGACTTTCTACTGCAGCAGACAAGACTTACCC AAGAGAGTTAATGGCAAAGATATACAATACA
ESTD-		:	1	GCCGCAATGCCCGGGAGTTTCTCCAATGTGTGGAGAAGGCCTTAGAAGACATGTTTGATGCCTTAGAAGGCAAATCCATCAAAAGGTTAGAAAGGTTAGAAAGGTTAGAAAGGTTAGAAAGGTTAGAAAGGTGAAAAGGTGGAAGGCAGAGGCAGGC

				ATGCTTGCCTTGGATTTCAGCGGCACAAGGCTCAGCTGAACCTGGCTACCAGGACCTGGCCTGCAC
ESTD				TCTCCTGTTTTTCTTCTCTTCATCCCTGTCTTCTGCAAAGCAATGCACGTGGCCCAGCCTGTGTGTG
				CAGGCCAGCGTGGTGGTGGTCACCATCCCGGCAGAGAACAGGTCAGCCACCACTATGCACAGGT
CYP2D6 :-	1	:		TCTCATCATTGAAGCTGCTCTCAGGGTTCCCCTTGGCCTGAGCAGGGCCCGAGAGCATACTCGG
				AAAAAAACATTTTAACACCTTTTCAATCATATACACCATAAATTTCCATTTTTCACATAAGTCAGTT
		<u> </u>		TGAGCTGAGTTTTCCAATTACTTGCAATCTAAAATGTCATAACTGATTAATGCAAGTTCAACAGACA
ESTD-				ACTTTCCCAAGCATCTACGATCAGAAGGTCAAAATATTACATATCTGGATTAAATTATGCCCATAT
D11S1873	:	•		CTGCATGTC
				CATOCOCAAGOCCATCCTCTAGOCACTGGCATTTTTGCCGCCTCTGACAGATACACTCAGGGCCGT
				CATGCTGCACACATOCAGGGGGGCGCCCTACCCTTTGTAGTCCATGGGAAAGGCTCCTCTGGGGCGGTG
ESTD				GGGTTGTGTGGCTATGTGGTGGTCTTGTGTAGACGGGGCTTTGGTTTCAGTTGCACTATTGCGTTATT
D17S33	:	•	•	GCAGATTGCTTTGCACCTGAGCGAGCCTC
			•	TTTGAGACCACCTGGCCAACATGGCGAAATCACATCTCTACCAAAATTACAAAATTAGCTGGGTGT
				GGTGGTACATGCCTATCGTAATCCCAGCTACATCGGGAGGCTGAGGCAGGAGAATTGCTTGAACCCA
ESTO				GGAGGCAGAGCTTGCAGTGAGCCAAGATCACACCACTGCACTTACAGCCTGGGTGACACAGTGGAGA
D18S8	1 1	Ī	,	CTCTGTCTCAA
				AACTGATTAGAACCTGAAAATACATATTTTATCTGAAAAAGTCGAGTTATTGGCTCATCACATTGG
				AATITTTGCATCATTAAAAAATCCAATAAAGTACACTGTAATAAAGAATTTAACAGAATATCATTGT
ESTD		,		TTATTCAAACTATTTATCACTTATTTATTGGTAAGCCATACTAAATTCTAAAGCATGTTTCTGAAAG
D3S11	;		,	TTTA
				AGGITICCACATTATTGCTGATGTTTGCTGATGTTTCCAGGAGCCTTGATGTCATTCTGTATCTCCTCAG
ESTO		-		GTATCCCACCTTGAGACGTACTTTTCAAAACTCTCTACAGCCGTTGTTGTTATTAATTCAAGGTTGA
D3S12		1		ACATAAAGTA
				GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCCTGC
				TGAGTCTTATTCAAAACTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTCCC
ESTO				AGAAGTGAAACATACTGCTCCTAGAAGOCAGAGTCATACTGGATGTTCTGTTTCGGTCTTCACGATGG
D3S2	- 	:	1	CAGGTATGAAATATAATCTGTCCTTTATTTGGAAGGATGCCGGTATGT
				TTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATATGAAATGTATT
				CTTAAACAATAAACTTGAAAGTCCAAAATTACTCCTTGATCCATGGACTGCAGAATAAATGTTATTT
ESTD				TAGCTGTCAGAAAACAATACTAATCTTGCATATGTTCATCAGAGCCCTTGGGTGACCAGGTGTATT
D4S338	-	:		GCCAATAAGCAGTAATATTTTGAGGGAATCTTGTTTTCAATGCAGTAG
ESTO				CTTTCATGCACGATAGGCTTTCTCTACTAATCACAGAATTTTGAGAAGAAGAAAAAAACAACTTTCAAGG
D4S95			:	ATAATGGGGCAATCACTTTCTTTCTTTAGAGTCTACCGG

ESTD					TGAATCTTAATTGCTATCTCTACAAAATGTATAAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGAGCCAGTCTCCTACAATCATCTTCACAAACATTTTCATCCATGGACTCCATACTAGAAAACATTTTC
D7S399	:		:	;	GIEGGEGACACCACGCTCCAGGCTGGGCCTTGCACGTGTGGCTCAAGCAGCTGCTCGGCTCCACT
					TCCATGGGTGTGGGGCCTGGGACCTCACTGTCCCTGGGGGAGAGGAGGAGGGGGGGG
Fermon	:				GAATGCTGATTACTGGTGGGGGGGGGGGGGGAACATGGGGGGGG
					TCCCCAGCCCTATCGGTCATTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAACCCATCAC
සු					ACAAAACGGTCAGCACCCAACCTGAACTCGCAGATGCTGDCACACATGCTCATGCCAAAAGCT
Ö	:	1	1		AGAGGAGATTGCTCTGGGGCTCGCTATTAAGAAACTAAGGTAC
	-				TCTGCCTTTGGTGCAGGAGGCTGCCCGGCGAGCCGGAGCTGGAGATGGAGATGCTCTCCAGCACA
		_			GOCCACOCGAGAGGACCOGGTACAGCCCCATCCCACCAGCCACCACCACCTGACTCTCCCCGACCG
ESTID					TCCCADCACGGTCTCCACAGCACTCCCGACAGCCGCCAAACCAGAGAAGAATGGGCATGCCAAAG
0802	_:	;	:		ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
		F			AAGACGATGGCCAGGATGAGCGCGCAGTAGGAGAGGCCATAGTAGGCATGTGGGGCGGGGCTGGCT
FSTD					CACCTGTGGAGTTCTCTGCCCCACAGGTGTAGTTCAGGTGGCCACTCAGCTGGCTCAGAGATGCCATA
0803	:	<u>;</u>	<u>;</u>	:	GOCCAGAGGGAGGTGCTGATGCCAAGGGGCTTCCTGTGAGGAGA
	_				TCTTTCAGGATCOGCATCTGCGCCTGGGTTGGGCATCGCTCCGCTAGGTGTCAGCGGCTCCACCAGCTGG
ESTO					GGTGAGGGGGTGATGGGTCAGTGCCGGGGCCCGGTGCAGACCCCACGCGGGGCTGGGAGGACTTCACCC
5885	:	<u> </u>	:	•	CGCCTCACCTCCGCTTTCCTGCAGCAGTCTCCGCATCGTGGTACT
	_	F			ACTCACAGTGCTTTTAAGTGAAAATGGTCGAGAAAGAGGCACCAGGAAGCCGTCCTGGCGCTGGCA
					GTCCGTGGGACGGGATGGTTCTGGCTGTTTGAGATTCTCAAAGGAGCGAGC
es es					AGACTATTTTAGATTTTCTTTTGCCTTTTGCAACCAGGAACAGCAAATGCAAAAACTCTTTGAGAGG
28	<u>:</u>	+	1	:	GTAGGAGGGTGGGAAGAACAACCATGTCATTTCAGAAGTTAGTT
	L				GATAAGTACACTGAGGCCCCAGGAGGTTATTGCCTAGTAGCCCAACTGTGCATGCA
		_			GCACCAAATGGCCTCCAAGGCCCGTAGGGGAACTGGGGGGATCTAGGGGATGGGTGAGGAATGGCCC
		_			AGOCCAGTCCCGGGGGGGGGGGGGGGGGGGGGGGGCCGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
ESTD-F2	:				TGGATGAG
		F			AGATCCTGATGATTTTTTTCCTATTTTTTCTAAATGTTTTACAGTTTGAAGTTTTAGATTTATGCCCA
					TGCTCCATTTTGAGTTAATATTTGTGTAAAGTATGATGTTTAAGTCAAACTTCATTTTTTTCCATA
ESTD-F9	:	<u>_</u> ;			GGTATGTCCAATTTATCCAGCACAATTTGTTAAAACAAAAAC

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	_			CGCAGACCGGTCAGTGTGGGGTCGGGAGTGTGTGTGAAGGAAG
	_			TTCCGGGGTGACTTTCCCGTTCTGTGCTTGCAGAGAGGCGGGGAGACACAGAGAGCACAGAGTGGCTAA
ESTO				GTGTAAGGGACCTCTGGTCGCACCGTGTTCTGCTGCCCCTGTTCAGCTGTCTGT
	1	•	•••	CTCTGTCCCGGAAATTCCGAGAGCT
				GTTTATGCATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCCTGGTCACCATGAC
				AACCACAGGGCCTCTCAGGAACACAGTAAGCCCTGGCAGGAGAATCCCCCCACCCCACACCTGGCTGG
				ABCAGGAAATGOOGAGOGGOGOOTGAGOOOCCAGGGAAGCAGGCTAGGATGTGAGAGACACAGTCACC
ESTD-GCK :-	1			TGCAGCCTAATTACTCAAAAGCTGTCCCCAGGTCACAG
esap			-	GACCTGAGTACCTCCTAGTGAGCAAGATGTGCTCCGATCCAGGGTCAAAACCACAGGCATCATTG
GNAT2				AAACCAAGTTTTCCGTCAAAGACTTGAATTTCAGGTAAGTGCATGGTTCCCTAGG
ESTD				
GPPK2L	:	·		AGTCTTCATCTGCGGTGTCCAGGTAGATCCCTTTCACCGCCGAGAACTGCTCGATATC
ESTD.				CTGGGCTOGOOOGCAGCAGCTGCTGGCACCTGGACGGCGCGCCAGGCTCACCTCTATAGTGGGGGTCG
HPAS ::	<u> </u>			TATTCGTCCACAAAATGCATCTGGATCAGCT
				TTGGAAAGTTCTCCACTGTTAACCCAGTCTATGTTGGCAATGTGGCCTGGGCCCACATTCTGGCCTTG
				AGGGCCCTGCAGGACCCCAAGAAGGCCCCAAGCATCCGAGGACAGTTCTACTATATCTCAGATGACA
ESTO				CGCCTCACCAAAGCTATGATAACCTTAATTACACCTGAGCAAAGAGTTCGGCCTCCGGCTTGATTCC
HSD3B1				AGATGGAGCTTTCCTTTATCCCTGATGTATTGGATTGGCTTCCTGCTG
				GGGCTAAAATTTCCGAGCAACTTTGCATAGACTGTTTTATTTGACTTGACAGGATTGCTAGAGATAGG
				CAGGGAGAGGAGGATGTGTTACAGTTTGTCAGAGAATAAAAAGGATAACCTGGGGTTTTCTGTGC
				TITIGCTTCTTCACATCCCTGGGGAGTTAATAGCTGCAATTTTTCAAAGAACGGTATACAGGGACAGCA
ESTD-HT2				AAGCGCAGTCGTGAAGTTTCAAACAAGACACCCTT
				ACCAACGAGCCGCGATACAGACACTCTTAAGTTTTGCCCTAAGGCTCATTCAAATCATTAGGCATTTT
				CTGATAAACTAGGTTCTTGGGTGCCTTCTATCGGCAAGAATGCGTACTTATTTGAATAGTAGAGGTAA
				ACCACACGCCCCAAGAGTCACTGACTGGCAGCTTCTGCAGCAGGCGTGAACCCCCGTAGCCTAAA
ESTD-HT4	:	•		TGACAGCCGAAGAGGCGCCGAAGACATGCGCGC
				AACACACAAGCCCCAGCGAGAATTGAACTCGCGACCCTGGTTTACAAGACCAGTGCTCTAACCCCT
				GAGCTATGGAGCCCTCGTCGCTGTTGGTTTTTCTTCCTTTCATCTTATAGATTGATGTTATGCTCCTA
				GCATTCCGGCTACCGAATAGGATGTTAGCTTGAGTAAAATTCCAGGATATTCTCCTACAAAATGAAA
ESTD-HTS	:			ACATITICGIGCTCIGIAAATCCCTCGAAAAGGTTCT
ESTD				ACCCAGTGGAGCCGCTCATTGCACGGTCTTGGCAGGAGGTGCCCTGGGAGAAGAAGAAGAAGATGTTC
GFBP1	1		:	CAGGGCACACATAGCTTAGTGGAGACTC

ESTO-			TTTACTATTICAATGGATACAGAATTGTGGGAGTCACTATATTCCTATGAACAAAAATTCAGATTT CAGTGTTAAGTAATGTTGCCTACATTGTGAGTGACGGGCCAGTGGTGGATCCGAGAGTGTGGTGGG TGCACGGACATAATGAGTAAGCAATATGGAAAGATGAGTATCTATGGATACGAACTGAAAGT
IGHV4-6	11		AIGIAAAIACIICACAAAAIACIACAAAAAAAAAAAAAA
			CAAAGTAAGCACCCAATAAATGTTAGCIATIAVIATICATICATICATICACTGCACTGCACTTGGCACTCTGGCACTCTGGAGTGCAATGTCGGCTCACTGCAAGCTCTG
			CCTCCTGGGTTCATGCCATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGAATACAGGCACCACT
4 ii 0		-	GTTCCCGGCTAATITTTTGTATTTTAGTAGAGCGGAGTTCACCGT
ESID-ILIA ::			CCACTTACAGATGGATAAATGGGTACAATGAAGGGCCAATAGCCCTCCCT
ESTD-IL18	;		GGGTCTCTACCTTGGGTGCTGTTCTCTCTGAGGGCTCTGTCAATTGCAGG
			CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTTACCTTTTGGCAATATT
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			GGGGAGTAAAACTTGGATTGGGAGATTTCATTTTCTACAGTGTTCTGGTTGGT
			GCCAGTGGAGACTGGAACACACATAGCCTATTTCGTAGCCATATTAATTGGTTTGTGCCTTACATT
	-		ATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAGCTCTTCCAATCTCCATCACCTTTGGGCTTGTTTT
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: 		;	TTCTGAAAATCATGGTCCCTAGAACATTTTGTAAAGAGGTAAGTCTTATGAAATTATAATCTT
			ACCTACABAGGTGGCTGGATGGTGTGTCCAACQCGAGGAATCTGAGAGGCGAGAGGGGGGTGGCTG
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				CCATGACTGGGATGCTAAGTCAGCAACTGAGTTCATTCAT
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ESTD-TAT	<u>:</u> ;	-	•	GAGAAGCAAATTTTAAATAGGACCCAIGAGACACAICA
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	_ : ;	<u> </u>	:	CACTGGATTGGCCCAAACAAGTCTGAGTGCCAGCCAGGACTCAACAGTCCCTGGATTGGCCCAAAGTCAGGACTCAACAGTCAGAACTCAACAGAACTCAACAGAACTCAACAGAACTCAACAGAACTCAACAGAACTCAACAGAACTCAACAGAACTCAACAGAACTCAACAGAACTCAACAGAACTCAACAGAACTCAACAGAACTCAACAGAACTCAACAGAACTCAACAGAACTCAACAGAACTCAACAGAACTCAACAGAACTCAACAGAACTCAACAGAACTCAACAGAACTCAACAGAACTCAACAGAACTCAACAGAACTCAACAGAACTCAACAGAACTCAACAGAACTCAACAGAACTCAACAGAACTCAACAGAACTCAACAGAACTCAACAGAACTCAACAGAACTCAACAGAACTCAACAGAACTCAACAGAACAACAACAACAACAACAACAACAACAACAACA
				TTCCTGCATCCTGTCTGGAAGTTAGAAGGAAACAGACACAGAGACCTGGTCCCCAAAAGAAATGGAGG
				CAATAGGITTTGAGGGCATGAGGACGGGGTTCAGCCTCCAGGGICCIACACACAGAAICAGICAGIC
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				CAAGGCAGAAAAGCTGGTGCTTCATGGGCAAAATCAATGTCTCTCCCAGAIIICAGAILCCCCAAAAICAAA
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			TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTTCTTACAACATCAAGGGTCTGTTGTTTTTTTT
			GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAGGTCACAGAGACAGGAAACACAAGTG
ESID			<u>ACTCTGAGATGTCACCAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCGGGGCATG</u>
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			AGGTAGGAAAAGCAAAGAGTTGATTAGTGAAGGAGAGAGA
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			CGACGTGTGCCTGGAGTAGCCCCGACTCTTGTACGGTCGGCATCTGAGACCAGTGAGAAACGCCCTT
ESTD-WT1	:	1	CATGTGTGCTTACCCAGGCTGCAA
			TTGGGAAGTTAGAGCCTATATTAAATTACGGAATTACTAAGGCAGGACACAGAGGCTTAATTGAAAA
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1			TCT
			AGCACCACCTCTCACGTCAAGCCTCAGCACCAGATGCTGTTCTATAAGGATGACGTGCTGTTTTACAA
			CATCTCCTCCATGAAGAGCACAGAGAGTTATTTATTCCTGAAGTCCGGATCTATGACTCAGGGACAT
EST71770			ATAAATGTACTGTGATTGTGAACAACAAGAAGAAAACACTGCAGGAGTACCAGGTGTTGGTGGTGGAAGG
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			CCAGTGAGCAGCAACAGGGCCAGGGCTGGCTTATCAGCCTCCCAGCCCAGACCTGGCTGCAGACAT
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		-	GGGACAAGGTCAACTCCTTCTTCAGCACCTTCAAGGAGAAAGAGAGAG
FST51976			COCTGAGCTGGAGCAACAGCAGGAACAGCAGCAGGAGCAGCAGCAGGAGCAGGAGCAGGTGCAGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT
-			CCTTTGGAGAGCTGCCCTGGTGC

EST11458			CCACTTTGGTAGTGCCAGTGTGACTCATCACAATGATTTCTCCAGTGCTCATCTTGTTCTCCAGTTTTCCCAGTTTTCCCAGTGTTCCCCAGTGGTCCCCAGTGGTTTTCCACAGTGGTGGTCCCCATTAAAACATTCTATGAGCCAGGAAAAAAATACTGCCCATTAAAAAAATTTTATGAGCCAGGAAAAAAATTCTGCCCCATGACAATTCTTATGTGCCCTCTCAACAACTTGCCCCTTTATTTTTCTGCCCTCTCCAGGACTGTGGCC
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EST36027			AGTGACTTCCAAGGAAATGGCTACCCAACTTGCTTCATGCGCCTGCTGGCCAACTATGCCTCTCAGAACATGCAAAACGTGCAAAAACGTGAAAAAGGGACTCACAACAACAGAAAAGGGAATGCATACATGATGATGATGATGATGATGATGATGATGATGATGATGA
ST12274			COCCCAGTTGACAGOCACTGCTCTAGACTAAGTTTCTTGCTTCCAAATAGAGCCTTACCAAAGTGTAT TACATAAAGAAGTCAAGTGGTTTTACTCCTCATGACCAAATATTCTTTCCCTCCTTAGGATGAGGTGA TAGTAAATGACCGATGGGGTCAGAACTGTTCCTGTCACCATGGAGGATACTATAACTGTGAAGATAA ATTCAAGCCACAGAGGTTGCCAGTC
======================================			ATGCTAAGGGGATCGGACATGAAAGGACCCTGTGAGCCGATTGTCCTATCTCCAGCGGCCCTGTCATC CAGCTCACTCATCAATGGGGCCAGTCAGGCCACTGGGCTCCGGAGGAGGACTCACCACTGCCCCT GCTGCCATGTGGACTGGTGCAAGTTGAGGACTTCTTG
EST44438	7		GCAGOCAGGAGOGGCTGCAOCATGCCCGCATAGATGCGGACCTCAAGCTCGACTTCAAGGACGTCCT GCTCCGAOCTAAGCGGAGCAGCCTCAAGAGCCGAGGCGAGG
EST12839			TGCAAAACACACAAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCCTCTTTGCT CCTAACATCTATGTACTGGATTATCTAAATGAAACACAGCAGCTTACTCCAGAGATCAAGTCCAAGG CCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAGTAAGAGAAACTTGAATGTTATTCAACTGG
EST54419	:	1	CTTCTGCCTAATTTGAATGATATGTTGCTGTGGGACCTGAGCACTTTTATGGCACAAATGATCACTA TTTTCTTGACCCCTACTTACAATCCTGGGAGATGTTTGGGTTTAGCGTGGTCGTATGTTGTCTACTA TAGTCCAAGTGAA
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			TGCTTGGGGTGGCAAAGAACAAGGAGGGAGGAGGAGGAGGAGGGTTTTATGAAGGGGGGG
EST10398			AGATGCTGCCACCTCTTATCTACTTGATGTTCACATTTGGGGCTTGACTTTCCAACACGGAGAAG
			CATTGTTTCTTCGGGCCAAGAAGGTATCTACCAATAGTGTCTATTAGGCATTTG
EST36751		!	CCAAGTCGTTCAATTTTAGCTTTGCAGGTTTTAACTCGATTACTTTTTCTATTCAAATCTCTGTAAAA TTGAAATATGAACTTAGTTTTCTGATCTATGGTTTCAAGTTAAACAG
			CACGIGGAAAGGAGCTATTTIGGAGGCTTTAAGAGAAATATTTACCTTTGAAAAATAATG
EST40562		!	AGGATITGACCICCITCGCTCTGGAAGAGTATCCGTACCGTA
			GCTCTCTATACCCCTGTGGTCCTCCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAAAACTGAAAAACTGAAAAACTGAAAAACTGAAAAAACTGAAAAAACTGAAAAAAAA
EST18288		1	ACAGCACCTGGCTTTCAACACCTACGTCCACTTCCAAGGTAAGGCAAACCTCTGCTGGCTCTGGC CCTAGGACTTAGTATCC
			TTCCCGCCAGCCCCCATCCTTGGCACCCTGGTCCCCTCAGGGGCCCACCCCGCGGGGCACTCACCGCTCT
EST70523			CECTCTCEGIAACATCCGGCCGGCGGCCTCCTTGAGCACATAGCCTGGACCGTTTCCGTATAGGAGG ACCGTGTAGGCCTTCCTGTCCCGGGGCCTTGCCAGGGGCCCTGCAGAGAGGGGGTCCCTGTGGT
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			ATCGAAATGTATTTTCATTGAGAACACCAATATTACAGTTTGTGCTTTCCATTATGAGTCCCAAAAT
EST36770			TCAACCCTCCCGATAGGGCTGGGCCTGAACAAAATATACGGGTTTCCTGTTTCCTTTTCGAGGCTTAACAAGTTATA

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			CCATAAAGTAATTTTGTGAAAGAAGGAGCAAGAACATTCCTCTGCAGCACTTCACTACAATGA
EST26021	<u> </u>	1	GCATTAGCTACTTTTCAGAATTGAAGGAGAAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTTCTTTCCTTTTGCAACAAGACAAAGCAAAGCC
			ATCCTGAGCTCGCCAATAAGCTTCTTGGTTCTACTTCTCTTCTCCACAAGGCCCCAATTCACTTTCTCAGGGGAAATCCCAAGAGGCCCTTGGAGCCTTTGTGCTCCCACTCAATACAAAAAGGCCCTCTTGTGCTCCCACTCAATACAAAAAGGCCCCTCTTGTACACACTCAATACAAAAAGGCCCCTCTTAACAAAAAGGCCCCTCTTAACAAAAAAAA
			GTTCCGAATCCTCCTCCAAAGTGGCCGGGTTTAATCTGCTCATGACGCTGCGGCTGTGGTCCAGCT GAGGTGAGGGGGCTTGAAGCTGGGAGTGGGGGTTTAGGGACGCGGGTTTGGGGTGCATCTGCGTGCATCAAGCTCT CAAAAAAAAAA
EST20118	!	:	CTGAGA
EST53018		i	ACAATCCAGGTCACACATTCCAGAAGAGGAGGGGTGGTCAGTGAGCCTGGGTAGGTCCAGTAATCCA AGGATTCAGGAAGGAGCCACGAGGATCGAAGTTAGTGAAGTC
			CTTCCTATGGGATTTGACTTTATTTTCTCCATTGTCTTACCTTTTACAGGTGTTAATATAGTGAAAAGGAAACGTGCAGTCATGACAGTTTGAAAGTTTGACAATTACACAAGAAGGAAATAAAT
EST68787	<u>!</u>		AGAATCAAGCACTTTCGAAACATTGAAGTTGTTTTGAACTTGGTGTCACCTTTAATTACAACCTAG CAGACGGAACTGAACT
EST34088			GTGGGGGCAACAGTGGGAAAAGGGGCCAAGGGTATAAAAGGGGCCAACAAAAGAGGCGCTCAAGG ATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCCTGTGGACAGCTCACCTAGCTGCAATGGCTACA
:	1	:	GGIVAG
EST37382			CTGAGAAACATTGGCAAAATAAAGGAATTTGGCACTCCCCACCCCCTCTTCTCTTCTCTTCTGTTGGACTTGAGGAACTGGGCCTGAACTGAGCAAGAAGAAAGA
			TOCAGGGTGGCTGGAOOOCAGGOOOCAGCTCTGCAGCAGGGAGGAOGTGGCTGGGGCTCGTGAAGCATG
			TGGGGGTGAGOOCAGGGGGOOCAAGGCAAGGGAALLIGAGLI ILAALLIGAGLIGAGIGAGGGGGGGGGG
EST74082	:	:	TGGGGACCTGACCCAGCCATTGTGAACCAACACCTGTGCG
			GOCCTCCTCTTCCAATTCTGTCCCTATAGTTTTCCTCTATTAAGTGAACTACATGCATTCTTTTAGT
			GGATAGATGCACACACACACACGCCATTATGGGGAAGGATCCACGTGTGTGT
EST45311		•	CATACACATCTGTGTGTTGTGAAT

		TGCCCCATCACGCGGCCGAGACATGGCTTGCCACAGCTCTTGAGGATGTCACCAATTAACCAGAAAT
EST65258		CAMATTATTT HUMALUST CAMANTGACAGCCAGGCCGGCCGGGTGCTTCTGGGGGCTCGTCGGGGGGGG
ECT20046	:	GTTAGGTGCGTGTTTCCTGTGCAAGTCAGGACATCAGTCTGATTAAA
3	!	ATGCAGGATGAAGGTGGACAGGGAGGAGGGCCAACCTGTCATCCCAGGGCCTGCAGATGTCGCTG
		ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATTATTAGCATTTGTTTAGCATTACCTAA
		TITITITICTICCTCCATGCAGACTGTTAGCTTTTACCTTAAATGCTTATTTTAAAATGACAGTGGAAG
EST62782	:	
		GAGATCGGTGTGAGTTATTAGGCATGGTTACCTGTGATTCTCCCAATCTTGTGCGTTCCACCGATG
E31338/8		GAACTGCCGGCAAATCCTGACAAGTGTGCACCCAGGCTGTACCCAATTAGGTGAACATGGCTTCGAG
		ACANA I I CANADA I I CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CA
EST68308		GCTGAGTTACAACACAATACTTTACAATACTTTTTTTTTT
:	***	GAAGTAGACTTTAAAGGTAAGAAAGTAGTTATTTTA GAAGTAGACTTTAAAGGTAAGAAAGTAGTTATTTTA
	-	GGAATATTAAAAATATTTAAAATACCTCCATTTTGCTTATCCTTTTAGTGAAGATGATACCTGCAA
		AAGACATGGCTAAAGTTATGATTGTCATGTTGGCAATTTGTTTCTTACAAAATCGGAAGTCT
	:	GITAAGTAAGTACTGTTTGCCTTGGAATTGGATTTTAATGTTGACTTTATCAT
EST52908		ATCACAGGTCTCTGGTCTCTGGCCATCATTTCCTGGGAGAGATGGATG
:	:	CAATGTGAGATTTGATG
004050		AGGAGAAGCTGAGGAAGGAGAGAGAGAGAATGACATTGATGAGAGATGTCGGCTCAGGAT
	::	GCCGGAAANTGAC
		TGAAGCTTCTGCCCAGCTTGCATTGTTTCTAGGAGAACCCGCGTCATACCTTTATCTATAGCCTTCCCC
EST/6136	:	TAGGTCTT
		CTCTGGATGGGTTCACAGGTGGCAGGCACAGCCAGTCCATCCTGTAGTCATCATAGTTTGTTGACTCC
		CAAGITGCTCTCCTCACTGGAGAACAAGGACAGCCACATGGCGGGATGGCCGGGGAGTTCTGGT
ES158607		TGCGGCCACGGCTGTGGCCTCGTTGTGAACGGTAGCCTTTGCGGTTGCGATGCCTAAACCTTTGTTCT
		TGGCCAAGGAGGGGGGGGGGCATGCCTGAGATGTAGATGCGGCC
		Legend: 1=Marker 2=PM Position 3=Reference Allele 4=Altered Allele 5=SNP Forward Primer
		6=SNP Reverse Primer 7=Sequence

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EQUIVALENTS

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that

5 various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described specifically herein. Such equivalents are intended to be encompassed in the scope of the claims.

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CLAIMS

WE CLAIM:

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- A nucleic acid segment shown in column 7 of the Table, or a portion thereof which includes a polymorphic site, or the complement of the segment or portion thereof.
- 2. The nucleic acid segment of claim 1 that is DNA.
- 3. The nucleic acid segment of claim 1 that is RNA.
- 4. The segment of claim 1 that is less than 100 bases.
- 5. The segment of claim 1 that is less than 50 bases.
- 10 6. The segment of claim 1 that is less than 20 bases.
 - 7. The segment of claim 1, wherein the polymorphic site is biallelic.
- 8. The segment of claim 1, wherein the polymorphic form occupying the polymorphic site is the reference base for the fragment listed in the Table, column 3.
 - 9. The segment of claim 1, wherein the polymorphic form occupying the polymorphic site is an alternative form for the fragment listed in the Table, column 4.
 - 10. An allele-specific oligonucleotide that hybridizes to a segment of a fragment shown in the Table, column 7 or its complement.
 - 11. The allele-specific oligonucleotide of claim 10 that is a probe.

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- 12. The allele-specific oligonucleotide of claim 10, wherein a central position of the probe aligns with the polymorphic site of the fragment.
- 13. The allele-specific oligonucleotide of claim 10 that isa primer.
 - 14. The allele-specific oligonucleotide of claim 13, wherein the 3' end of the primer aligns with the polymorphic site of the fragment.
- 15. The allele-specific oligonucleotide of Claim 10, which is selected from the group consisting of the nucleotide sequences of the Table, column 5.
 - 16. The allele-specific oligonucleotide of Claim 10, which is selected from the group consisting of the nucleotide sequences of the Table, column 6.
- 15 17. An isolated nucleic acid comprising a sequence of the Table, column 7 or the complement thereof, wherein the polymorphic site within the sequence or complement is occupied by a base other than the reference base shown in the Table, column 3.
- 20 18. A method of analyzing a nucleic acid, comprising obtaining the nucleic acid from an individual; and determining a base occupying any one of the polymorphic sites shown in the Table.
- 19. The method of claim 18, wherein the determining
 comprises determining a set of bases occupying a set of
 the polymorphic sites shown in the Table.

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20. The method of claim 18, wherein the nucleic acid is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and the method further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.